

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:00:15 ; Search time 187 Seconds
(without alignments)
14.098 Million cell updates/sec

Title: US-10-719-523-5
Perfect score: 48
Sequence: 1 HHHHHH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	48	100.0	6 2 AAAY49221	AAy49221 Nickel to
2	48	100.0	6 2 AAM19161	AAy19161 Isoelectr
3	48	100.0	6 2 AAM18225	AAy18225 Purificat
4	48	100.0	6 2 AAM63024	AAw63024 Hexa-hist
5	48	100.0	6 2 AAM69961	AAw69961 Poly-His
6	48	100.0	6 2 AAM68297	AAw68297 Poly-His
7	48	100.0	6 2 AAM44011	AAw44011 Poly-His
8	48	100.0	6 2 AAE08742	AAe08742 Poly-His
9	48	100.0	6 2 ADV42333	Adv42333 Hexahisti
10	48	100.0	6 2 AAy06469	AAy06469 Epitope t
11	48	100.0	6 2 AAM84203	AAw84203 Peptide c
12	48	100.0	6 2 AAy17447	AAy17447 Major out
13	48	100.0	6 2 AAy09544	AAy09544 Human TAK
14	48	100.0	6 2 AAy33592	AAy33592 VH-VL dom
15	48	100.0	6 2 AAE16561	AAe16561 Epitope t
16	48	100.0	6 2 AAy50711	AAy50711 Single ch
17	48	100.0	6 3 AAy78351	AAy78351 His-6 pep
18	48	100.0	6 3 AAy99641	AAy99641 His6 tag
19	48	100.0	6 3 AAB08438	AAB08438 Histidine
20	48	100.0	6 3 AAy78346	AAy78346 His-6 pep
21	48	100.0	6 3 AAy77706	AAy77706 6-His pep
22	48	100.0	6 3 AAy96951	AAy96951 Polyhisti
23	48	100.0	6 3 AAB10788	AAB10788 B. subtil
24	48	100.0	6 4 AAB59857	AAB59857 6-His pep

25	48	100.0	6 4 AAE12713	AAe12713 Hexahis t
26	48	100.0	6 4 AAE13079	AAe13079 Epitope t
27	48	100.0	6 4 AAB35439	AAb35439 Nascent p
28	48	100.0	6 4 AAB45989	AAb45989 Transdomi
29	48	100.0	6 4 AAG78043	AAg78043 6-His epi
30	48	100.0	6 4 AAB97353	AAb97353 6-His epi
31	48	100.0	6 4 AAM52173	AAm52173 Peptide t
32	48	100.0	6 4 AAB76820	AAb76820 His tag.
33	48	100.0	6 4 AAB66801	AAb66801 6-His epi
34	48	100.0	6 4 AAE01997	AAe01997 Poly-His
35	48	100.0	6 4 AAG65669	AAg65669 His tag u
36	48	100.0	6 4 AAU00163	AAU00163 His Tag t
37	48	100.0	6 4 AAG62605	AAg62605 Metal cap
38	48	100.0	6 4 AAB62662	AAB62662 C-termina
39	48	100.0	6 4 AAU02090	AAU02090 His-tag p
40	48	100.0	6 4 AAB85699	AAB85699 Amino aci
41	48	100.0	6 4 ABR00924	ABr00924 Hexahisti
42	48	100.0	6 4 AAE08006	AAe08006 His tag u
43	48	100.0	6 4 AAM51720	AAm51720 FSH alpha
44	48	100.0	6 5 AAE26107	AAe26107 His tag p
45	48	100.0	6 5 AAE28476	AAe28476 6His pep
46	48	100.0	6 5 AAM49702	AAm49702 KpnI/Sali
47	48	100.0	6 5 AAU10567	AAU10567 Purificat
48	48	100.0	6 5 AAG32021	AAg32021 Synthetic
49	48	100.0	6 5 AAE23795	AAe23795 His6 tag
50	48	100.0	6 5 AAE28606	AAe28606 His pep
51	48	100.0	6 5 AAO22927	AAo22927 Human pap
52	48	100.0	6 5 AAU76910	AAU76910 C termina
53	48	100.0	6 5 AAU75289	AAU75289 His6 tag
54	48	100.0	6 5 AAE18829	AAe18829 His tag u
55	48	100.0	6 5 AAO19983	AAo19983 Histidine
56	48	100.0	6 5 AAG93013	AAg93013 Synthetic
57	48	100.0	6 5 AAG32856	AAg32856 His tag f
58	48	100.0	6 5 AEG71813	AEg71813 His tag p
59	48	100.0	6 5 AEB77485	AEb77485 AAV-heipe
60	48	100.0	6 5 ADG70469	ADg70469 Histidine
61	48	100.0	6 5 AAG98509	AAg98509 Synthetic
62	48	100.0	6 6 ADA05147	ADa05147 Peptide s
63	48	100.0	6 6 AAE30397	AAe30397 6-His tag
64	48	100.0	6 6 AAO16087	AAo16087 Neurologi
65	48	100.0	6 6 AEP55464	AEp55464 Peptide s
66	48	100.0	6 6 AAO16240	AAo16240 Synthetic
67	48	100.0	6 6 AAO16698	AAo16698 PAL-781 p
68	48	100.0	6 6 AEM32676	AEm32676 Histidine
69	48	100.0	6 6 AEP55533	AEp55533 Adapter p
70	48	100.0	6 6 AEP58182	AEp58182 Hexa-hist
71	48	100.0	6 6 AEU58805	AEu58805 Mucin 1 (
72	48	100.0	6 6 AEU08057	AEu08057 Synthetic
73	48	100.0	6 6 ABR40361	ABr40361 Hexahisti
74	48	100.0	6 6 ABj38460	ABj38460 6-His epi
75	48	100.0	6 6 AEP58380	AEp58380 Histidine
76	48	100.0	6 6 AAE34362	AAe34362 His tag u
77	48	100.0	6 6 AEG73745	AEg73745 His-tag #
78	48	100.0	6 6 AEU08700	AEu08700 Protein a
79	48	100.0	6 6 AAE34693	AAe34693 His tag p
80	48	100.0	6 6 AEU55850	AEu55850 His tag p
81	48	100.0	6 6 AEU93302	AEu93302 Single ch
82	48	100.0	6 6 AEU08159	AEu08159 Synthetic
83	48	100.0	6 6 AEU09877	AEu09877 Six histi
84	48	100.0	6 6 AAE30831	AAe30831 His tag p
85	48	100.0	6 6 AEP56478	AEp56478 Interfero
86	48	100.0	6 6 AAE32846	AAe32846 His-tag p
87	48	100.0	6 6 ABR83551	ABr83551 Fusion pr
88	48	100.0	6 6 ADA94904	ADa94904 Interfero
89	48	100.0	6 6 ADB25838	ADb25838 His6x epi
90	48	100.0	6 7 ABR62463	ABr62463 Poly-hist
91	48	100.0	6 7 ADA09805	ADa09805 His6x epi
92	48	100.0	6 7 ADB16593	ADb16593 Poly-His
93	48	100.0	6 7 ADB87317	ADb87317 Polyhisti
94	48	100.0	6 7 ADC64741	ADc64741 Hepatiti
95	48	100.0	6 7 ADC73007	ADc73007 Poly-His
96	48	100.0	6 7 ADC78273	ADc78273 Poly-His
97	48	100.0	6 7 ADD28984	ADd28984 His tag.

98	48	100.0	6	7	ABM01458	Abw01458	Hexa-hist	171	48	100.0	6	8	ADT91376	Adt91376	Hexahisti
99	48	100.0	6	7	AD656097	Ad656097	Corticotr	172	48	100.0	6	8	ADT71347	Adt71347	Marker pe
100	48	100.0	6	7	AD624170	Ad624170	N-termina	173	48	100.0	6	8	ADT91518	Adt91518	His6 tag
101	48	100.0	6	7	AD651383	Ad651383	CRF2 non-	174	48	100.0	6	8	ADT88255	Adt88255	His tag p
102	48	100.0	6	7	ABW02158	Abw02158	Histidine	175	48	100.0	6	8	ADT78164	Adt78164	C. pneumo
103	48	100.0	6	7	ADP44382	Adt44382	Epitope t	176	48	100.0	6	8	ADU48662	Adu48662	His tag a
104	48	100.0	6	7	ADP50719	Adt50719	Furin pep	177	48	100.0	6	8	ADU48596	Adu48596	Amino aci
105	48	100.0	6	7	ADP53324	Adt53324	Adeno-as8	178	48	100.0	6	8	ABY00768	AbY00768	Poly-hist
106	48	100.0	6	7	ADP70394	Adt70394	Orphan re	179	48	100.0	6	9	ADV24178	Adv24178	Nickel ma
107	48	100.0	6	7	ADG32337	Adg32337	His6 tag	180	48	100.0	6	9	ADV24326	Adv24326	Nickel ma
108	48	100.0	6	7	ADG98833	Adg98833	His-6x (h	181	48	100.0	6	9	ADV24212	Adv24212	Nickel ma
109	48	100.0	6	7	ADG84817	Adg84817	Corticotr	182	48	100.0	6	9	ADV24579	Adv24579	Nickel ma
110	48	100.0	6	7	ADG46728	Adg46728	Poly-His	183	48	100.0	6	9	ADV24675	Adv24675	Nickel ma
111	48	100.0	6	7	ADH44350	Adh44350	Transfect	184	48	100.0	6	9	ADU92041	AdU92041	His tag,
112	48	100.0	6	7	ADH69235	Adh69235	6x-His ta	185	48	100.0	6	9	ADU92529	AdU92529	6-His epi
113	48	100.0	6	7	ADH63030	Adh63030	His tag u	186	48	100.0	6	9	ADV98592	Adv98592	Novel chi
114	48	100.0	6	7	ADH53325	Adh53325	His tag p	187	48	100.0	6	9	ADM38214	AdM38214	Histidine
115	48	100.0	6	7	ADH54589	Adh54589	His tag u	188	48	100.0	6	9	ADM09034	AdM09034	His-6 pep
116	48	100.0	6	7	ADH96360	Adh96360	Ineulin r	189	48	100.0	6	9	ADM64949	AdM64949	6-His epi
117	48	100.0	6	7	ADH80639	Adh80639	Rana pipi	190	48	100.0	6	9	ADM23846	AdM23846	Novel hum
118	48	100.0	6	7	ADJ59015	Adj59015	Amino aci	191	48	100.0	6	9	ADM10847	AdM10847	His tag.
119	48	100.0	6	7	ADK41227	Adk41227	G-CSF rel	192	48	100.0	6	9	ADM26206	AdM26206	Human E44
120	48	100.0	6	7	ADM64594	Adm64594	TANGO197	193	48	100.0	6	9	ADM25792	AdM25792	Cleavable
121	48	100.0	6	8	ADP12240	Adp12240	Transfect	194	48	100.0	6	9	ADW22486	Adw22486	His6 tag
122	48	100.0	6	8	ADG45048	Adg45048	Synthetic	195	48	100.0	6	9	ADW96889	AdW96889	Histidine
123	48	100.0	6	8	ADP77118	Adp77118	Hexahisti	196	48	100.0	6	9	ADX57833	AdX57833	N-termina
124	48	100.0	6	8	ADG28807	Adg28807	Protein s	197	48	100.0	6	9	ADX05063	AdX05063	His tag p
125	48	100.0	6	8	ADH22658	Adh22658	Oligohist	198	48	100.0	6	9	ADX40948	AdX40948	His tag p
126	48	100.0	6	8	ADJ19013	Adj19013	His tag u	199	48	100.0	6	9	ADY27309	AdY27309	His epi t
127	48	100.0	6	8	ADJ34697	Adj34697	Amino aci	200	48	100.0	6	9	ADX85209	AdX85209	6x-His ta
128	48	100.0	6	8	ADJ23664	Adj23664	Hisx6 tag	201	48	100.0	6	9	ADY28266	AdY28266	His tag p
129	48	100.0	6	8	ADJ25161	Adj25161	Histidine	202	48	100.0	6	9	ADX87288	AdX87288	Protein p
130	48	100.0	6	8	ADJ36217	Adj36217	Self-coal	203	48	100.0	6	9	ADY50198	AdY50198	His tag p
131	48	100.0	6	8	ADJ36641	Adj36641	Protein p	204	48	100.0	6	9	ADY39758	AdY39758	His tag.
132	48	100.0	6	8	ADJ88139	Adj88139	His tail	205	48	100.0	6	9	ADY56834	AdY56834	Histidine
133	48	100.0	6	8	ADJ88087	Adj88087	Epitope-t	206	48	100.0	6	9	ADY34113	AdY34113	His tag p
134	48	100.0	6	8	ADJ79526	Adj79526	Hexa-hist	207	48	100.0	6	9	ADY34114	AdY34114	His tag p
135	48	100.0	6	8	ADJ50909	Adj50909	IGF-beta-	208	48	100.0	6	9	ADY53282	AdY53282	6xHis tag
136	48	100.0	6	8	ADL69051	Adl69051	IGF-1R/IR	209	48	100.0	6	9	ADY75189	AdY75189	Chlamydia
137	48	100.0	6	8	ADJ67712	Adj67712	fragment	210	48	100.0	6	9	ADY80247	AdY80247	Amino aci
138	48	100.0	6	8	ADL81220	Adl81220	6x-HIS ep	211	48	100.0	6	9	ADY75177	AdY75177	Hexa-hist
139	48	100.0	6	8	ADJ93827	Adj93827	Lysophosp	212	48	100.0	6	9	ADY78382	AdY78382	Histidine
140	48	100.0	6	8	ADN92353	Adn92353	S pneumon	213	48	100.0	6	9	ADZ03629	AdZ03629	Epitope t
141	48	100.0	6	8	ADM38896	Adm38896	His tag.	214	48	100.0	6	9	ADZ08744	AdZ08744	Recombina
142	48	100.0	6	8	ADM80159	Adm80159	Binding r	215	48	100.0	6	9	ADZ46754	AdZ46754	6-His tag
143	48	100.0	6	8	ADK13663	Adk13663	His tag.	216	48	100.0	6	9	ADZ59474	AdZ59474	Preferred
144	48	100.0	6	8	ADM94772	Adm94772	His tag f	217	48	100.0	6	9	ADZ69433	AdZ69433	Hexa-His
145	48	100.0	6	8	ADN06306	Adn06306	Hexahisti	218	48	100.0	6	9	AEA14985	AdE14985	6x-His ep
146	48	100.0	6	8	ADN06948	Adn06948	Poly-Hist	219	48	100.0	6	9	ADZ76889	AdZ76889	Fusion pa
147	48	100.0	6	8	ADN32452	Adn32452	6-His epi	220	48	100.0	6	9	ADZ69864	AdZ69864	His-tag f
148	48	100.0	6	8	ADN49511	Adn49511	Hexa-hist	221	48	100.0	6	9	ADZ87785	AdZ87785	Novel COP
149	48	100.0	6	8	ADN04650	Adn04650	His-tag p	222	48	100.0	6	9	ADZ85112	AdZ85112	Synthetic
150	48	100.0	6	8	ADN014230	Adn014230	Histidine	223	48	100.0	6	9	AEA23267	AdE23267	6x-His ta
151	48	100.0	6	8	ADN049029	Adn049029	Labelling	224	48	100.0	6	9	AEA99867	AdE99867	His tag.
152	48	100.0	6	8	ADN26659	Adn26659	Synthetic	225	48	100.0	6	9	AEA21312	AdE21312	Nanoparti
153	48	100.0	6	8	ADN26661	Adn26661	Synthetic	226	48	100.0	6	9	AEBO0924	AdE00924	Hexahisti
154	48	100.0	6	8	ADP84150	Adp84150	E. coli c	227	48	100.0	6	9	AEB13397	AdE13397	His tag s
155	48	100.0	6	8	ADP90806	Adp90806	Protein/p	228	48	100.0	6	9	AEBA4084	AdE44084	His tag p
156	48	100.0	6	8	ADP87523	Adp87523	Arrr asso	229	48	100.0	6	9	AEBS5912	AdE55912	6xHis tag
157	48	100.0	6	8	ADN08828	Adn08828	Histidine	230	48	100.0	6	9	AEB70210	AdE70210	Hexahisti
158	48	100.0	6	8	ADQ96748	Adq96748	6-His pur	231	48	100.0	6	9	AEB68294	AdE68294	Epitope t
159	48	100.0	6	8	ADN03293	Adn03293	Epitope-t	232	48	100.0	6	9	AECC0178	AdE00178	His6 epi t
160	48	100.0	6	8	ADQ98113	Adq98113	Peptide	233	48	100.0	7	1	AAp80401	AdA80401	Affinity
161	48	100.0	6	8	ADRI6247	Adi6247	His tag p	234	48	100.0	7	2	AAV03173	AdV03173	Human car
162	48	100.0	6	8	ADP90374	Adp90374	Histidine	235	48	100.0	7	4	AA664363	AdA64363	Peptide i
163	48	100.0	6	8	ADR29322	Adr29322	Histidine	236	48	100.0	7	5	AAE14511	AdE14511	Tag added
164	48	100.0	6	8	ADS20226	AdS20226	His tag p	237	48	100.0	7	5	AAE25397	AdE25397	His tag p
165	48	100.0	6	8	ADR88395	Adr88395	6-histidi	238	48	100.0	7	6	AAER83552	AdE83552	Fusion pr
166	48	100.0	6	8	ADR72506	Adr72506	Dehydroge	239	48	100.0	7	6	ABU61988	AdB61988	Synthetic
167	48	100.0	6	8	ADR39718	Adr39718	His tag p	240	48	100.0	7	8	ADH23659	AdH23659	Oligohist
168	48	100.0	6	8	ADSI17887	Adsi17887	Peptide t	241	48	100.0	7	8	ADH58901	AdH58901	6xHis tag
169	48	100.0	6	8	ADR72483	Adr72483	Peptide p	242	48	100.0	7	8	ADQ49030	AdQ49030	Labelling
170	48	100.0	6	8	ADS74281	AdS74281	6xHis tag	243	48	100.0	7	9	ADY34115	AdY34115	Hy tag pe

244	48	100.0	7	9	ADZ69281	Ad69281 Hexahisti	317	48	100.0	8	9	ADY67556	Ady67556 His tag.
245	48	100.0	7	9	AEB34466	Aeb34466 Exemplary	318	48	100.0	8	9	ADZ04230	Adz04230 Modified
246	48	100.0	7	9	AEC10134	Aec10134 Histidine	319	48	100.0	8	9	ADZ39458	Adz39458 Histidine
247	48	100.0	8	2	AAR77412	Aar77412 Extension	320	48	100.0	8	9	AEB17922	Aeb17922 Peptide u
248	48	100.0	8	2	AAR95439	Aar95439 Polymisti	321	48	100.0	8	9	AEB24522	Aeb24522 N-termina
249	48	100.0	8	2	AAW20036	Aaw20036 C-termina	322	48	100.0	8	9	AEB86406	Aeb86406 Amino aci
250	48	100.0	8	2	AAW61479	Aaw61479 A. fumiga	323	48	100.0	8	9	AEB71113	Aeb71113 C-Adi Kin
251	48	100.0	8	2	ABU61601	Abu61601 polymisti	324	48	100.0	8	9	AEB30728	Aeb30728 Therapeut
252	48	100.0	8	3	AAV53237	Aav53237 MN protei	325	48	100.0	8	9	AEB91052	Aeb91052 Lantibiot
253	48	100.0	8	3	AAW03014	Aaw03014 Tag fused	326	48	100.0	9	2	AAW06142	Aaw06142 Variant a
254	48	100.0	8	3	AAW09991	Aaw09991 C. tetani	327	48	100.0	9	2	AAW60080	Aaw60080 Homo sapi
255	48	100.0	8	3	AAV96685	Aav96685 Polymisti	328	48	100.0	9	2	AAV28306	Aav28306 Amino aci
256	48	100.0	8	3	AAW00161	Aaw00161 Hexahisti	329	48	100.0	9	2	AAW90199	Aaw90199 B7-2-6His
257	48	100.0	8	4	AAE13200	Aae13200 His tag u	330	48	100.0	9	3	AAV53258	Aav53258 Human neu
258	48	100.0	8	4	AAW36993	Aaw36993 Peptide u	331	48	100.0	9	3	AAV44463	Aav44463 Gly(His)8
259	48	100.0	8	4	AAW64364	Aaw64364 Peptide i	332	48	100.0	9	3	AAV79558	Aav79558 Peptide t
260	48	100.0	8	4	AAW52174	Aaw52174 Peptide i	333	48	100.0	9	3	AAW15187	Aaw15187 His-conta
261	48	100.0	8	4	AAW48167	Aaw48167 Histidine	334	48	100.0	9	4	AAE13114	Aae13114 C-termina
262	48	100.0	8	4	AAE08227	Aae08227 Tag #1 fo	335	48	100.0	9	4	AAW82692	Aaw82692 His-tag.
263	48	100.0	8	4	AAU00164	Aau00164 His Tag (336	48	100.0	9	4	AAW64361	Aaw64361 Peptide i
264	48	100.0	8	4	AAW64395	Aaw64395 Peptide t	337	48	100.0	9	4	AAV97661	Aav97661 Influenza
265	48	100.0	8	4	AAE11985	Aae11985 Tag #2, t	338	48	100.0	9	5	AAO18574	Aao18574 E coli ou
266	48	100.0	8	4	AAW51721	Aaw51721 FSH alpha	339	48	100.0	9	5	AAO19058	Aao19058 Mutation
267	48	100.0	8	5	AAU964775	Aau964775 Divinyl e	340	48	100.0	9	5	AAW70938	Aaw70938 Plasmodu
268	48	100.0	8	5	ABP53086	Abp53086 CYP 27C1	341	48	100.0	9	5	AAU09999	Aau09999 Nonapepti
269	48	100.0	8	5	AAU99814	Aau99814 Membrane	342	48	100.0	9	6	ABG72218	Abg72218 Polymisti
270	48	100.0	8	5	ABG32022	Abg32022 Synthetic	343	48	100.0	9	6	ABR27181	Abv27181 Human can
271	48	100.0	8	5	AAU78663	Aau78663 His tag e	344	48	100.0	9	6	ABP70232	Abp70232 Membrane
272	48	100.0	8	5	AAE31736	Abj31736 Fish grow	345	48	100.0	9	6	ABU89706	Abu89706 Poly-hist
273	48	100.0	8	5	AAE16245	Aae16245 Polymisti	346	48	100.0	9	6	ABR83554	Abv83554 Fusion pr
274	48	100.0	8	5	AAU77832	Aau77832 His tag p	347	48	100.0	9	6	ABR83544	Abv83544 C-termina
275	48	100.0	8	5	AAU77821	Aau77821 C terminal	348	48	100.0	9	7	ADB67705	Adb67705 Peptide 1
276	48	100.0	8	5	AAU99314	Aau99314 His6tag p	349	48	100.0	9	7	ADU99740	Adu99740 Honeybee
277	48	100.0	8	5	ABG71814	Abg71814 Peptide t	350	48	100.0	9	8	ABU64370	Abu64370 Llg/HyHEL
278	48	100.0	8	5	AAU99299	Aau99299 Brevibacti	351	48	100.0	9	8	ADH22661	Adh22661 Oligohisti
279	48	100.0	8	6	ABG73746	Abg73746 His-tag #	352	48	100.0	9	8	ADI82698	Adi82698 Vector pe
280	48	100.0	8	6	ABP56479	Abp56479 Interfero	353	48	100.0	9	8	ADJ50911	Adj50911 IFN-beta-
281	48	100.0	8	6	ABP71241	Abp71241 Histidine	354	48	100.0	9	8	ADU49032	Adu49032 Labelling
282	48	100.0	8	6	ABR83560	Abv83560 His6-Ser2	355	48	100.0	9	8	ADU16338	Adu16338 Human pro
283	48	100.0	8	6	ABR83553	Abv83553 Fusion pr	356	48	100.0	9	8	ADW94950	Adw94950 human apo
284	48	100.0	8	6	ADW94905	Adw94905 Interfero	357	48	100.0	9	8	ADY80248	Ady80248 Amino aci
285	48	100.0	8	6	ABU61986	Abu61986 Synthetic	358	48	100.0	9	9	AEA18561	Aea18561 Amino aci
286	48	100.0	8	7	ADC39944	Adc39944 Recombina	359	48	100.0	9	9	AEB24523	Aeb24523 N-termina
287	48	100.0	8	7	ADD67262	Add67262 His tag e	360	48	100.0	10	2	AAW39733	Aaw39733 First typ
288	48	100.0	8	7	ADD32211	Add32211 Plasmid p	361	48	100.0	10	2	AAW73684	Aaw73684 Metal-aff
289	48	100.0	8	7	ADP53514	Adp53514 Bacteriai	362	48	100.0	10	2	AAW77469	Aaw77469 I-domain
290	48	100.0	8	7	ADP93704	Adp93704 Tag pepti	363	48	100.0	10	2	AAW74672	Aaw74672 Polymisti
291	48	100.0	8	7	ADP86365	Adp86365 Human cyt	364	48	100.0	10	2	AAW31496	Aaw31496 Human DNA
292	48	100.0	8	7	ADH34464	Adh34464 Armb C-te	365	48	100.0	10	2	AAW56089	Aaw56089 Human mon
293	48	100.0	8	7	ADL01701	Adl01701 GUS beta-	366	48	100.0	10	2	AAW72331	Aaw72331 Protein a
294	48	100.0	8	7	ADK41228	Adk41228 G-CSF rel	367	48	100.0	10	2	AAW89262	Aaw89262 N-termina
295	48	100.0	8	8	ADP28865	Adp28865 His (6) t	368	48	100.0	10	2	AAV50501	Aav50501 Dermatoph
296	48	100.0	8	8	ADG45049	Adg45049 Syntheti	369	48	100.0	10	2	AAV06610	Aav06610 Hexahisti
297	48	100.0	8	8	ADH22660	Adh22660 Oligohist	370	48	100.0	10	2	AAW94259	Aaw94259 His-tag e
298	48	100.0	8	8	ADH17890	Adh17890 Caspase-7	371	48	100.0	10	2	AAV43534	Aav43534 Leishmani
299	48	100.0	8	8	ADH76464	Adh76464 Peptide o	372	48	100.0	10	2	AAW82996	Aaw82996 Human fib
300	48	100.0	8	8	ADJ77673	Adj77673 C-termina	373	48	100.0	10	3	AAV51518	Aav51518 Human TFR
301	48	100.0	8	8	ADK00112	Adk00112 His-tag w	374	48	100.0	10	3	AAW28976	Aaw28976 N-termina
302	48	100.0	8	8	ADO49031	Ado49031 Labeling	375	48	100.0	10	3	AAW90141	Aaw90141 Leader se
303	48	100.0	8	8	ADO98121	Ado98121 Peptide	376	48	100.0	10	3	AAW87721	Aaw87721 Leader se
304	48	100.0	8	8	ADR16114	Adr16114 SGH16 ta	377	48	100.0	10	3	AAW10776	Aaw10776 B. subcil
305	48	100.0	8	8	ADR16873	Adr16873 Ser-Gly-H	378	48	100.0	10	4	AAW10830	Aaw10830 Expressio
306	48	100.0	8	8	ADR30797	Adr30797 ADAM33 C-	379	48	100.0	10	4	AAW98321	Aaw98321 Recombina
307	48	100.0	8	8	ADR88396	Adr88396 Peptide u	380	48	100.0	10	4	AAU19104	Aau19104 His-Tag C
308	48	100.0	8	8	ADR49664	Adr49664 His tag p	381	48	100.0	10	4	AAW72220	Aaw72220 Histidine
309	48	100.0	8	8	ADT12574	Adt12574 Polymis p	382	48	100.0	10	4	AAV97658	Aav97658 Influenza
310	48	100.0	8	9	ADT61982	Adt61982 Human WSX	383	48	100.0	10	4	AAW70426	Aaw70426 Oligo-his
311	48	100.0	8	9	ADU92045	Adu92045 His tag.	384	48	100.0	10	4	AAW75181	Aaw75181 Recombina
312	48	100.0	8	9	ADM25793	Adm25793 Cleavable	385	48	100.0	10	5	AAE28471	Aae28471 ChimERIC
313	48	100.0	8	9	ADM78624	Adm78624 S. aureus	386	48	100.0	10	5	AAU97726	Aau97726 Epitope t
314	48	100.0	8	9	ADX18091	Adx18091 Peptide 1	387	48	100.0	10	5	ABW76374	Abw76374 Hexa-hist
315	48	100.0	8	9	ADY34118	Ady34118 HY tag pe	388	48	100.0	10	5	AAE28849	Aae28849 Peptide u
316	48	100.0	8	9	ADY34116	Ady34116 HY tag pe	389	48	100.0	10	5	ABW05988	Abw05988 Monoclonal

390	48	100.0	10	5	AU78933	Au78933	9	Histidi	463	48	100.0	11	8	AD57742	Ad57742	6x N-term
391	48	100.0	10	6	ABG75687	Abg75687	2C-methyl	464	48	100.0	11	8	AD76992	Ad76992	Poly-His	
392	48	100.0	10	6	ABG73909	Abg73909	His-tagge	465	48	100.0	11	8	ADN37757	Adn37757	Endoplasm	
393	48	100.0	10	6	ABR27276	Abt27276	Human can	466	48	100.0	11	8	ADO21902	Ado21902	Polyhisti	
394	48	100.0	10	6	ABR27717	Abt27717	Human can	467	48	100.0	11	8	ADO49034	Ado49034	Labelling	
395	48	100.0	10	6	ABP97469	Abp97469	Vector pT	468	48	100.0	11	8	ADP49312	Adp49312	Natriturec	
396	48	100.0	10	6	AAOI6174	AAOI6174	O6-alkylg	469	48	100.0	11	8	ADP49268	Adp49268	Natriturec	
397	48	100.0	10	6	ABB82902	ABb82902	Amino aci	470	48	100.0	11	8	ADP49285	Adp49285	Natriturec	
398	48	100.0	10	6	AAE30843	AAe30843	His tag p	471	48	100.0	11	8	ADP88411	Adp88411	Human int	
399	48	100.0	10	6	ABR83555	ABr83555	Fusion pr	472	48	100.0	11	8	ADRS0730	Adr50730	N-termi	
400	48	100.0	10	7	ADC72967	Adc72967	Peptide a	473	48	100.0	11	8	ADT07104	Adt07104	His tag p	
401	48	100.0	10	7	ADD68299	Adc72967	Peptide a	474	48	100.0	11	9	ADY34244	Ady34244	His tag p	
402	48	100.0	10	7	ADP28730	Adt28730	SUR2-type	475	48	100.0	11	9	ADY30851	Ady30851	His tag p	
403	48	100.0	10	7	ADP28734	Adt28734	SUR2-type	476	48	100.0	11	9	ADY54245	Ady54245	Modified	
404	48	100.0	10	7	ADP28735	Adt28735	SUR2-type	477	48	100.0	11	9	ADY54254	Ady54254	Modified	
405	48	100.0	10	7	ADP28731	Adt28731	SUR2-type	478	48	100.0	11	9	ADY54252	Ady54252	Modified	
406	48	100.0	10	7	ADP28733	Adt28733	SUR2-type	479	48	100.0	11	9	ADY60812	Ady60812	C-termi	
407	48	100.0	10	7	ADP28732	Adt28732	SUR2-type	480	48	100.0	11	9	AEA27993	AEA27993	Poly-His	
408	48	100.0	10	7	ABR83692	ABr83692	C-termi	481	48	100.0	11	9	AEA21677	AEA21677	Aspartate	
409	48	100.0	10	7	ADP88580	ADp88580	Protein t	482	48	100.0	11	9	ABE09678	ABe09678	Factor Xa	
410	48	100.0	10	7	ADH44345	Adh44345	Transfect	483	48	100.0	11	9	ABE87456	ABe87456	N-termi	
411	48	100.0	10	7	ADL61533	Adl61533	B. tauros	484	48	100.0	12	2	AAO7064	AAo7064	Transcrip	
412	48	100.0	10	7	ADL26635	Adl26635	Multi-mari	485	48	100.0	12	2	AAW61549	AAw61549	Endoprote	
413	48	100.0	10	7	ADL90486	Adl90486	C-termi	486	48	100.0	12	2	AAV15775	AAv15775	Histidine	
414	48	100.0	10	8	ADP12235	Adl12235	Transfect	487	48	100.0	12	2	AAW82993	AAw82993	Human fib	
415	48	100.0	10	8	ADG30367	Adg30367	His tag p	488	48	100.0	12	3	AAV53265	AAv53265	Pili coat	
416	48	100.0	10	8	ADH22662	Adh22662	Oligohist	489	48	100.0	12	3	AAV95878	AAv95878	Hexahisti	
417	48	100.0	10	8	ADJ77679	Adj77679	C-termi	490	48	100.0	12	4	AAH85050	AAh85050	Peptide t	
418	48	100.0	10	8	ADL33425	Adl33425	Bacterial	491	48	100.0	12	4	AAU04934	AAu04934	Human pla	
419	48	100.0	10	8	ADO05860	Ado05860	Peptide t	492	48	100.0	12	4	AAU04935	AAu04935	Human pla	
420	48	100.0	10	8	ADO49033	Ado49033	Labelling	493	48	100.0	12	4	AAH64365	AAh64365	Peptide i	
421	48	100.0	10	8	ADP49278	Adp49278	Natriturec	494	48	100.0	12	4	AAH72438	AAh72438	His tag.	
422	48	100.0	10	8	ADP90803	Adp90803	Protein/p	495	48	100.0	12	5	AAU96716	AAu96716	Molecular	
423	48	100.0	10	8	ADQ60109	Adq60109	His tag p	496	48	100.0	12	5	AAU96774	AAu96774	Divinyl e	
424	48	100.0	10	8	ADR29320	Adr29320	Histidine	497	48	100.0	12	5	ABB05983	ABb05983	Monoclon	
425	48	100.0	10	9	ADV23840	Adv23840	Linker co	498	48	100.0	12	5	AAE19655	AAe19655	Aridopos	
426	48	100.0	10	9	ADV23887	Adv23887	Novel fus	499	48	100.0	12	6	ABR33965	ABr33965	Plasmid p	
427	48	100.0	10	9	ADY34120	Ady34120	HY tag pe	500	48	100.0	12	6	ABP55084	ABp55084	Hexa-hist	
428	48	100.0	10	9	ADY34119	Ady34119	HY tag pe	501	48	100.0	12	6	ADA26429	Ada26429	Synthetic	
429	48	100.0	10	9	ADY34117	Ady34117	HY tag pe	502	48	100.0	12	7	ABB80260	ABb80260	Human big	
430	48	100.0	10	9	AEA14998	AEa14998	10X-His e	503	48	100.0	12	7	ADD95116	ADd95116	Human GBP	
431	48	100.0	10	9	ADZ69667	Adz69667	GCGS-His-	504	48	100.0	12	8	ADP28957	ADp28957	Nuclear r	
432	48	100.0	10	9	AEA18562	AEa18562	Amino aci	505	48	100.0	12	8	ADH22664	ADh22664	Oligohist	
433	48	100.0	10	9	ABE43913	ABe43913	Rhomboid	506	48	100.0	12	8	ADH53866	ADh53866	Human cel	
434	48	100.0	11	2	AAH77410	AAh77410	Extension	507	48	100.0	12	8	ADN02212	ADn02212	Vector pQ	
435	48	100.0	11	2	AAW61480	AAw61480	A. fumiga	508	48	100.0	12	8	ADL09056	ADl09056	Human big	
436	48	100.0	11	2	AAW53171	AAw53171	C-termi	509	48	100.0	12	8	ADO49035	ADo49035	Labeling	
437	48	100.0	11	2	AAW80426	AAw80426	Linker us	510	48	100.0	12	8	ADP88406	ADp88406	Human int	
438	48	100.0	11	2	AAV05815	AAv05815	Non-toxic	511	48	100.0	12	8	ADU59684	ADu59684	GBP-4 rel	
439	48	100.0	11	2	AAV42688	AAv42688	Polyhisti	512	48	100.0	12	9	ADV66855	ADv66855	Vector pP	
440	48	100.0	11	2	AAW70581	AAw70581	Amino aci	513	48	100.0	12	9	ADX40941	Adx40941	His tag p	
441	48	100.0	11	3	AAH1895	AAh1895	H3SA muta	514	48	100.0	12	9	ADZ03810	ADz03810	6His pep	
442	48	100.0	11	3	AAH09993	AAh09993	C. tetani	515	48	100.0	12	9	ADT76029	ADt76029	PTICAGAM	
443	48	100.0	11	4	AAE11753	AAE11753	Modified	516	48	100.0	12	9	ABE79153	ABe79153	Additiona	
444	48	100.0	11	4	AAH68981	AAH68981	Fluoresce	517	48	100.0	13	2	AAH72792	AAh72792	Hexa-hist	
445	48	100.0	11	5	AAU96727	AAu96727	Molecular	518	48	100.0	13	2	AAW61548	AAw61548	Endoprote	
446	48	100.0	11	5	AAE20416	AAE20416	His6G14YC	519	48	100.0	13	2	AAV05816	AAv05816	Non-toxic	
447	48	100.0	11	5	AAW50625	AAW50625	Polyhisti	520	48	100.0	13	3	AAV56262	AAv56262	Maedi-Vi	
448	48	100.0	11	5	ABG31725	ABg31725	Human PPA	521	48	100.0	13	3	AAH10782	AAh10782	B. subcil	
449	48	100.0	11	5	ABE76132	ABb76132	Modified	522	48	100.0	13	4	AAE13116	AAE13116	C-termi	
450	48	100.0	11	5	AAU97110	AAu97110	pAWG21-hu	523	48	100.0	13	4	AAH51258	AAh51258	pCONGAM H	
451	48	100.0	11	5	ABP52434	ABp52434	Histidine	524	48	100.0	13	4	AAE12152	AAE12152	Oligopept	
452	48	100.0	11	5	ABG70847	ABg70847	His-6 epi	525	48	100.0	13	4	AAH72415	AAh72415	Synthetic	
453	48	100.0	11	6	ABR42764	ABr42764	Suitable	526	48	100.0	13	4	AAH80820	AAh80820	His tag p	
454	48	100.0	11	6	ADA26448	Ada26448	Suitable	527	48	100.0	13	4	AAH80817	AAh80817	His tag p	
455	48	100.0	11	7	ADC42700	Adc42700	Modified	528	48	100.0	13	4	AAU09363	AAu09363	N-termi	
456	48	100.0	11	7	ADC81600	Adc81600	Modified	529	48	100.0	13	4	AAU09362	AAu09362	N-termi	
457	48	100.0	11	7	ADC81592	Adc81592	Modified	530	48	100.0	13	4	AAU09364	AAu09364	N-termi	
458	48	100.0	11	7	ABW00720	ABw00720	C-termi	531	48	100.0	13	4	AAU09365	AAu09365	N-termi	
459	48	100.0	11	7	ADH85798	ADh85798	His-tag p	532	48	100.0	13	5	ABG32366	ABg32366	Peptide u	
460	48	100.0	11	7	ADJ66025	Adj66025	Native Hi	533	48	100.0	13	5	AAU11045	AAu11045	Translate	
461	48	100.0	11	8	ADH22663	ADh22663	Oligohist	534	48	100.0	13	5	AAU11796	AAu11796	Peptide a	
462	48	100.0	11	8	ADT79358	Adt79358	6x His ta	535	48	100.0	13	6	ABG75997	ABg75997	Jellyfish	

536	48	100.0	13	6	ADA45512	Vector pE	609	48	100.0	15	6	ABR38536	Abt38536 Human can
537	48	100.0	13	6	ABP55018	Hexa-hist	610	48	100.0	15	6	ABR38508	Abt38508 Human can
538	48	100.0	13	6	ABP55083	Hexa-hist	611	48	100.0	15	6	ABR38402	Abt38402 Human can
539	48	100.0	13	6	ABU63441	His-tagge	612	48	100.0	15	6	ABR38453	Abt38453 Human can
540	48	100.0	13	7	ADP47860	Human alp	613	48	100.0	15	6	ABR38533	Abt38533 Human can
541	48	100.0	13	7	ADP28728	Ocxl tran	614	48	100.0	15	6	ABR64019	ABR64019 C-termina
542	48	100.0	13	7	ADP28724	Ocxl tran	615	48	100.0	15	6	ABR59491	ABt59491 His tag p
543	48	100.0	13	7	ADP28738	Ocxl tran	616	48	100.0	15	6	AAO23103	AAo23103 C-termina
544	48	100.0	13	7	ADP28725	Ocxl tran	617	48	100.0	15	6	ABE37706	ABe37706 Peptide #
545	48	100.0	13	7	ADP28726	Ocxl tran	618	48	100.0	15	6	ABU61520	ABu61520 Hepatitis
546	48	100.0	13	7	ADP28729	Ocxl tran	619	48	100.0	15	7	ADB68861	ADB68861 Additiona
547	48	100.0	13	7	ADP28727	Ocxl tran	620	48	100.0	15	7	ADC40526	ADc40526 Peptide t
548	48	100.0	13	7	ADL01702	GUS beta-	621	48	100.0	15	7	ADC46940	ADc46940 Peptide #
549	48	100.0	13	8	ADO21275	Poly hist	622	48	100.0	15	7	ADC98709	ADc98709 His tag-a
550	48	100.0	13	8	ADP84148	E. coli c	623	48	100.0	15	7	ADD26197	ADd26197 Histidine
551	48	100.0	13	8	ADP87521	Arar C-te	624	48	100.0	15	7	ADD15437	ADd15437 His tag a
552	48	100.0	13	8	ADU48659	H. infive	625	48	100.0	15	7	ADD35403	ADd35403 General m
553	48	100.0	13	9	ADY74754	Lic aptcam	626	48	100.0	15	7	ADD44367	ADd44367 Cardoxype
554	48	100.0	13	9	ADZ69728	Toxin sin	627	48	100.0	15	7	ADD96098	ADd96098 His tag p
555	48	100.0	14	2	AAE12159	Human hg-	628	48	100.0	15	7	ADZ76697	ADz76697 Recombina
556	48	100.0	14	2	AAE12159	Human hg-	629	48	100.0	15	7	ADZ76697	ADz76697 His pepti
557	48	100.0	14	2	AAE12159	Human hg-	630	48	100.0	15	7	ADZ76697	ADz76697 APRT reco
558	48	100.0	14	3	AAE12159	Human TRF	631	48	100.0	15	7	ADZ76697	ADz76697 Purifying
559	48	100.0	14	3	AAE12159	Human TRF	632	48	100.0	15	7	ADZ76697	ADz76697 His tag p
560	48	100.0	14	3	AAE12159	Human TRF	633	48	100.0	15	7	ADZ76697	ADz76697 His tag p
561	48	100.0	14	3	AAE12159	Human TRF	634	48	100.0	15	7	ADZ76697	ADz76697 His tag p
562	48	100.0	14	3	AAE12159	Human TRF	635	48	100.0	15	7	ADZ76697	ADz76697 His tag p
563	48	100.0	14	3	AAE12159	Human TRF	636	48	100.0	15	7	ADZ76697	ADz76697 His tag p
564	48	100.0	14	3	AAE12159	Human TRF	637	48	100.0	15	7	ADZ76697	ADz76697 His tag p
565	48	100.0	14	3	AAE12159	Human TRF	638	48	100.0	15	7	ADZ76697	ADz76697 His tag p
566	48	100.0	14	3	AAE12159	Human TRF	639	48	100.0	15	7	ADZ76697	ADz76697 His tag p
567	48	100.0	14	3	AAE12159	Human TRF	640	48	100.0	15	7	ADZ76697	ADz76697 His tag p
568	48	100.0	14	3	AAE12159	Human TRF	641	48	100.0	15	7	ADZ76697	ADz76697 His tag p
569	48	100.0	14	3	AAE12159	Human TRF	642	48	100.0	15	7	ADZ76697	ADz76697 His tag p
570	48	100.0	14	3	AAE12159	Human TRF	643	48	100.0	15	7	ADZ76697	ADz76697 His tag p
571	48	100.0	14	3	AAE12159	Human TRF	644	48	100.0	15	7	ADZ76697	ADz76697 His tag p
572	48	100.0	14	3	AAE12159	Human TRF	645	48	100.0	15	7	ADZ76697	ADz76697 His tag p
573	48	100.0	14	3	AAE12159	Human TRF	646	48	100.0	15	7	ADZ76697	ADz76697 His tag p
574	48	100.0	14	3	AAE12159	Human TRF	647	48	100.0	15	7	ADZ76697	ADz76697 His tag p
575	48	100.0	14	3	AAE12159	Human TRF	648	48	100.0	15	7	ADZ76697	ADz76697 His tag p
576	48	100.0	14	3	AAE12159	Human TRF	649	48	100.0	15	7	ADZ76697	ADz76697 His tag p
577	48	100.0	14	3	AAE12159	Human TRF	650	48	100.0	15	7	ADZ76697	ADz76697 His tag p
578	48	100.0	14	3	AAE12159	Human TRF	651	48	100.0	15	7	ADZ76697	ADz76697 His tag p
579	48	100.0	14	3	AAE12159	Human TRF	652	48	100.0	15	7	ADZ76697	ADz76697 His tag p
580	48	100.0	14	3	AAE12159	Human TRF	653	48	100.0	15	7	ADZ76697	ADz76697 His tag p
581	48	100.0	14	3	AAE12159	Human TRF	654	48	100.0	15	7	ADZ76697	ADz76697 His tag p
582	48	100.0	14	3	AAE12159	Human TRF	655	48	100.0	15	7	ADZ76697	ADz76697 His tag p
583	48	100.0	14	3	AAE12159	Human TRF	656	48	100.0	15	7	ADZ76697	ADz76697 His tag p
584	48	100.0	14	3	AAE12159	Human TRF	657	48	100.0	15	7	ADZ76697	ADz76697 His tag p
585	48	100.0	14	3	AAE12159	Human TRF	658	48	100.0	15	7	ADZ76697	ADz76697 His tag p
586	48	100.0	14	3	AAE12159	Human TRF	659	48	100.0	15	7	ADZ76697	ADz76697 His tag p
587	48	100.0	14	3	AAE12159	Human TRF	660	48	100.0	15	7	ADZ76697	ADz76697 His tag p
588	48	100.0	14	3	AAE12159	Human TRF	661	48	100.0	15	7	ADZ76697	ADz76697 His tag p
589	48	100.0	14	3	AAE12159	Human TRF	662	48	100.0	15	7	ADZ76697	ADz76697 His tag p
590	48	100.0	14	3	AAE12159	Human TRF	663	48	100.0	15	7	ADZ76697	ADz76697 His tag p
591	48	100.0	14	3	AAE12159	Human TRF	664	48	100.0	15	7	ADZ76697	ADz76697 His tag p
592	48	100.0	14	3	AAE12159	Human TRF	665	48	100.0	15	7	ADZ76697	ADz76697 His tag p
593	48	100.0	14	3	AAE12159	Human TRF	666	48	100.0	15	7	ADZ76697	ADz76697 His tag p
594	48	100.0	14	3	AAE12159	Human TRF	667	48	100.0	15	7	ADZ76697	ADz76697 His tag p
595	48	100.0	14	3	AAE12159	Human TRF	668	48	100.0	15	7	ADZ76697	ADz76697 His tag p
596	48	100.0	14	3	AAE12159	Human TRF	669	48	100.0	15	7	ADZ76697	ADz76697 His tag p
597	48	100.0	14	3	AAE12159	Human TRF	670	48	100.0	15	7	ADZ76697	ADz76697 His tag p
598	48	100.0	14	3	AAE12159	Human TRF	671	48	100.0	15	7	ADZ76697	ADz76697 His tag p
599	48	100.0	14	3	AAE12159	Human TRF	672	48	100.0	15	7	ADZ76697	ADz76697 His tag p
600	48	100.0	14	3	AAE12159	Human TRF	673	48	100.0	15	7	ADZ76697	ADz76697 His tag p
601	48	100.0	14	3	AAE12159	Human TRF	674	48	100.0	15	7	ADZ76697	ADz76697 His tag p
602	48	100.0	14	3	AAE12159	Human TRF	675	48	100.0	15	7	ADZ76697	ADz76697 His tag p
603	48	100.0	14	3	AAE12159	Human TRF	676	48	100.0	15	7	ADZ76697	ADz76697 His tag p
604	48	100.0	14	3	AAE12159	Human TRF	677	48	100.0	15	7	ADZ76697	ADz76697 His tag p
605	48	100.0	14	3	AAE12159	Human TRF	678	48	100.0	15	7	ADZ76697	ADz76697 His tag p
606	48	100.0	14	3	AAE12159	Human TRF	679	48	100.0	15	7	ADZ76697	ADz76697 His tag p
607	48	100.0	14	3	AAE12159	Human TRF	680	48	100.0	15	7	ADZ76697	ADz76697 His tag p
608	48	100.0	14	3	AAE12159	Human TRF	681	48	100.0	15	7	ADZ76697	ADz76697 His tag p

682	48	100.0	16	6	ABU15405	Protein e	755	48	100.0	18	7	ADH61128	Mouse son
683	48	100.0	16	7	ADH44349	Transfect	756	48	100.0	18	7	ADH54691	Mouse son
684	48	100.0	16	7	ADH44347	Transfect	757	48	100.0	18	7	ADL46283	Protein N
685	48	100.0	16	7	ADM34937	H1A bindi	758	48	100.0	18	8	ADO43153	Human int
686	48	100.0	16	7	ADM33704	H1A bindi	759	48	100.0	18	8	ADO39421	N-termina
687	48	100.0	16	8	ADP12237	Transfect	760	48	100.0	18	8	ADU26453	Peptide r
688	48	100.0	16	8	ADP12239	Transfect	761	48	100.0	18	8	ADW38678	N-termina
689	48	100.0	16	8	ADM28856	Bacterial	762	48	100.0	18	9	ADW25902	N-termina
690	48	100.0	16	8	ADL24430	Modified	763	48	100.0	18	9	ADW21602	C-termina
691	48	100.0	16	8	ADL24490	Human inc	764	48	100.0	18	9	ADX38956	Plasmid p
692	48	100.0	16	8	ADO58594	Flag/8Hts	765	48	100.0	18	9	ADZ76275	Mouse son
693	48	100.0	16	8	ADR29318	Hisridline	766	48	100.0	18	9	AEA04352	Small Exp
694	48	100.0	16	8	ADT94020	rFel d 1 f	767	48	100.0	18	9	ADZ76977	6H1s prot
695	48	100.0	16	8	ADU04613	CGS5698-0	768	48	100.0	19	2	AAW00339	Rec2 prot
696	48	100.0	16	9	ADM47934	H1s-tag p	769	48	100.0	19	2	AAW37707	C-termina
697	48	100.0	16	9	ADY53507	MUC1 grow	770	48	100.0	19	2	AAV43533	Leishmani
698	48	100.0	16	9	ABE19851	PAMG22-Hi	771	48	100.0	19	2	AAW98067	Streptoco
699	48	100.0	17	2	AAR37708	Delta14 S	772	48	100.0	19	3	AAV90748	Protease
700	48	100.0	17	2	AAR68977	PGE α -7HPR	773	48	100.0	19	3	ABH11078	S. pyogen
701	48	100.0	17	2	AAW03939	T2 pepcid	774	48	100.0	19	4	ABH49879	H1s tag S
702	48	100.0	17	2	ABB08913	TNF/hpi f	775	48	100.0	19	5	ABP56043	Negative
703	48	100.0	17	2	AAW95000	N-termina	776	48	100.0	19	5	AAW79390	H1s tag/E
704	48	100.0	17	3	AAH26262	N-termina	777	48	100.0	19	6	AAE37111	Peptide u
705	48	100.0	17	4	AAH99608	ERA bindi	778	48	100.0	19	6	ABR42595	Substrate
706	48	100.0	17	5	ABH79628	Hexa-hist	779	48	100.0	19	6	ABE36602	Substrate
707	48	100.0	17	6	ABU63437	Thrombin	780	48	100.0	19	6	ABG73908	H1s-tagge
708	48	100.0	17	6	ADE24165	Plasmodiu	781	48	100.0	19	6	ABU61781	Synthetic
709	48	100.0	17	7	ADG17892	Adg17892	782	48	100.0	19	7	ADM64739	Hepaticis
710	48	100.0	17	8	ADK51966	Repeat pr	783	48	100.0	19	7	ADM78575	PRSET B v
711	48	100.0	17	8	ADK51960	Repeat pr	784	48	100.0	19	8	ADI25167	Saxiphilli
712	48	100.0	17	8	ADJ50913	IFN-beta-	785	48	100.0	19	8	ADR05296	N-termina
713	48	100.0	17	8	ADU04999	F. hepari	786	48	100.0	19	8	ADY53556	Truncated
714	48	100.0	17	8	ADS20742	TAP N-ter	787	48	100.0	19	9	AEA10606	Polo-like
715	48	100.0	17	8	ADX83549	Periphera	788	48	100.0	19	9	ABE91051	Lantibiot
716	48	100.0	17	9	AEA04353	Small Exp	789	48	100.0	20	2	AAR73014	N-termina
717	48	100.0	18	2	AAH60253	Vector-en	790	48	100.0	20	2	AAW00869	T-cell re
718	48	100.0	18	2	AAH69814	Site reco	791	48	100.0	20	2	AAW01445	Bioislaeci
719	48	100.0	18	2	AAH78152	Synthetic	792	48	100.0	20	2	AAW08594	Leader se
720	48	100.0	18	2	AAH95870	CR2 recep	793	48	100.0	20	2	AAV33454	Chemirc
721	48	100.0	18	2	AAW73374	Eptlope t	794	48	100.0	20	3	AAH80347	N-termina
722	48	100.0	18	3	AAH11047	Staphyloc	795	48	100.0	20	3	AAH83783	Poly (H1s)
723	48	100.0	18	3	AAH23253	Hexahisti	796	48	100.0	20	3	AAH87744	Human and
724	48	100.0	18	3	AAH10856	pSecrta-V	797	48	100.0	20	3	AAH28485	Human
725	48	100.0	18	4	AAH14660	Peptide #	798	48	100.0	20	4	AAE08579	N-termina
726	48	100.0	18	4	ABH333620	Peptide #	799	48	100.0	20	4	AAH70818	D3SD3-FLA
727	48	100.0	18	4	AAH27079	Peptide #	800	48	100.0	20	4	AAH82670	MBP/BMP f
728	48	100.0	18	4	ABH28438	Peptide #	801	48	100.0	20	4	AAH850878	Recombina
729	48	100.0	18	4	AAH97657	Influenza	802	48	100.0	20	4	AAH85139	Integrin
730	48	100.0	18	4	AAH05390	N-termina	803	48	100.0	20	4	AAH85140	Sequence
731	48	100.0	18	4	AAH35455	Clostridi	804	48	100.0	20	4	AAH85142	Sequence
732	48	100.0	18	4	AAH19075	Protein #	805	48	100.0	20	4	AAH85141	Sequence
733	48	100.0	18	4	AAH66794	Human bon	806	48	100.0	20	4	AAH85143	Sequence
734	48	100.0	18	4	AAH85750	Mouse son	807	48	100.0	20	4	AAH59137	N-termina
735	48	100.0	18	4	AAH54393	Human bra	808	48	100.0	20	4	AAH73436	N-termina
736	48	100.0	18	4	ABG48462	Human liv	809	48	100.0	20	5	ABH94460	H1s tag p
737	48	100.0	18	4	AAH73440	C-termina	810	48	100.0	20	5	ABH76190	Modified
738	48	100.0	18	4	AAH02383	Peptide #	811	48	100.0	20	5	AAO21570	Murine To
739	48	100.0	18	5	ABG36449	Peptide #	812	48	100.0	20	6	ABP59406	Self-abse
740	48	100.0	18	5	ABH79149	Human pep	813	48	100.0	20	6	ABP59407	Self-abse
741	48	100.0	18	5	ABH54919	Recombina	814	48	100.0	20	6	ABH83203	Membrane
742	48	100.0	18	6	AAH36641	Muonolysi	815	48	100.0	20	6	ABH63483	H1s tag p
743	48	100.0	18	6	ABU09400	Peptide #	816	48	100.0	20	6	AAE36646	Peptide #
744	48	100.0	18	6	ABU09938	Cytochrom	817	48	100.0	20	6	ABH64018	N-termina
745	48	100.0	18	6	ADA26288	Hedgehog-	818	48	100.0	20	6	ABR59490	H1s tag p
746	48	100.0	18	6	ABR81957	L. acidop	819	48	100.0	20	6	AAO23102	N-termina
747	48	100.0	18	7	ADD25294	Hedgehog	820	48	100.0	20	6	AAE37705	Peptide #
748	48	100.0	18	7	ADD25308	N-termina	821	48	100.0	20	6	ABH62029	Modified
749	48	100.0	18	7	ABW00879	Poly (H1s	822	48	100.0	20	7	ABH68860	Additiona
750	48	100.0	18	7	AAE39986	Peptide e	823	48	100.0	20	7	ADC40525	Peptide t
751	48	100.0	18	7	ADD71417	Mouse son	824	48	100.0	20	7	ADC46939	Peptide t
752	48	100.0	18	7	ABW01686	PolyH1s 1	825	48	100.0	20	7	ADC98708	H1s tag-a
753	48	100.0	18	7	ADH02816	Plasmid p	826	48	100.0	20	7	ADD26196	Hisridline
754	48	100.0	18	7	ADG73574	H1s tag-t	827	48	100.0	20	7	ADD15436	H1s tag a

828	48	100.0	20	7	ADD35402	901	48	100.0	21	2	AAV18411	AAy18411	Apomilgren
829	48	100.0	20	7	ADBS5530	902	48	100.0	21	2	AAV06793	AAy06793	Myc-His P
830	48	100.0	20	7	ADDP6097	903	48	100.0	21	2	AAW95646	AAw95646	c-Myc onc
831	48	100.0	20	7	ADSF6596	904	48	100.0	21	2	AAW92257	AAw92257	Myc-His-t
832	48	100.0	20	7	ADSF9814	905	48	100.0	21	2	AAV07741	AAy07741	Human bre
833	48	100.0	20	7	ADSF6494	906	48	100.0	21	2	AAW977132	AAw977132	AAy977132
834	48	100.0	20	7	ADSF6699	907	48	100.0	21	2	AAW86030	AAw86030	Myc-His P
835	48	100.0	20	7	ADSF6827	908	48	100.0	21	2	AAW95563	AAw95563	Myc-His t
836	48	100.0	20	7	ADG36770	909	48	100.0	21	2	AAW25329	AAy25329	Myc-His-t
837	48	100.0	20	7	ADG17903	910	48	100.0	21	2	AAV13472	AAy13472	Myc-His t
838	48	100.0	20	7	ADH13050	911	48	100.0	21	3	AAZ62127	AAz62127	Human TGF
839	48	100.0	20	7	ADG75196	912	48	100.0	21	3	AAZ26857	AAz26857	N-terminu
840	48	100.0	20	7	ADH69237	913	48	100.0	21	3	AAZ28465	AAz28465	OB gene-r
841	48	100.0	20	7	ADH48561	914	48	100.0	21	3	AAZ87743	AAz87743	Human and
842	48	100.0	20	7	ADH06299	915	48	100.0	21	3	AAZ28484	AAz28484	OB gene-r
843	48	100.0	20	7	ADJ62225	916	48	100.0	21	3	AAZ29273	AAz29273	Human pro
844	48	100.0	20	8	ADSF1038	917	48	100.0	21	3	AAV90318	AAy90318	Human pro
845	48	100.0	20	8	ADSF18061	918	48	100.0	21	4	AAE13185	AAe13185	Peptide u
846	48	100.0	20	8	ADJ32488	919	48	100.0	21	4	AAE07326	AAe07326	Myc-His t
847	48	100.0	20	8	ADJ83275	920	48	100.0	21	4	AAE08052	AAe08052	Myc-His t
848	48	100.0	20	8	ADK00358	921	48	100.0	21	4	AAU04210	AAu04210	Myc-His t
849	48	100.0	20	8	ADJ74084	922	48	100.0	21	4	AAO05538	AAo05538	Human pol
850	48	100.0	20	8	ADJ62024	923	48	100.0	21	5	AAE21826	AAe21826	Myc-His t
851	48	100.0	20	8	ADJ62027	924	48	100.0	21	5	AAO19089	AAo19089	Human psi
852	48	100.0	20	8	ADH96810	925	48	100.0	21	5	AAE22592	AAe22592	Peptide #
853	48	100.0	20	8	ADH99715	926	48	100.0	21	5	AAO21842	AAo21842	Breast ti
854	48	100.0	20	8	ADP70100	927	48	100.0	21	5	AAO19171	AAo19171	Human pro
855	48	100.0	20	8	ADJ78336	928	48	100.0	21	5	AAE21835	AAe21835	Myc-His t
856	48	100.0	20	8	ADJ25326	929	48	100.0	21	5	AAZ79563	AAz79563	Porato ps
857	48	100.0	20	8	ADJ59365	930	48	100.0	21	5	ABZ76276	ABz76276	Myc-His t
858	48	100.0	20	8	ADJ080039	931	48	100.0	21	5	ABP53471	ABp53471	SELPK re
859	48	100.0	20	8	ADJ081639	932	48	100.0	21	5	AAE26119	AAe26119	Myc-His t
860	48	100.0	20	8	ADJ58857	933	48	100.0	21	5	AAE22697	AAe22697	Myc-His t
861	48	100.0	20	8	ADJ48619	934	48	100.0	21	5	AAW50815	AAw50815	Mys-His P
862	48	100.0	20	8	ADJ48605	935	48	100.0	21	5	AAU80152	AAu80152	MyChis ta
863	48	100.0	20	8	ADJ15891	936	48	100.0	21	5	AAE21869	AAe21869	Myc-His t
864	48	100.0	20	8	ADJ94389	937	48	100.0	21	5	ABG68926	ABg68926	Lawsonia
865	48	100.0	20	8	ADJ08306	938	48	100.0	21	5	AAU75380	AAu75380	Immunotox
866	48	100.0	20	8	ADP98706	939	48	100.0	21	5	ABW84133	ABw84133	Ob protei
867	48	100.0	20	8	ADJ51716	940	48	100.0	21	6	ABU12328	ABu12328	Myc-His P
868	48	100.0	20	8	ADJ90322	941	48	100.0	21	6	ABU08632	ABu08632	LS147 pol
869	48	100.0	20	8	ADJ08031	942	48	100.0	21	6	ABG73776	ABg73776	Myc-His t
870	48	100.0	20	8	ADJ14640	943	48	100.0	21	6	ABP97471	ABp97471	Vector pe
871	48	100.0	20	8	ADJ080750	944	48	100.0	21	6	ABU64578	ABu64578	Obese (ob
872	48	100.0	20	9	ADJ43433	945	48	100.0	21	6	ABG99191	ABg99191	Guanylate
873	48	100.0	20	9	ADJ22621	946	48	100.0	21	6	ABU08597	ABu08597	Myc-His t
874	48	100.0	20	9	ADJ38677	947	48	100.0	21	6	ABU92017	ABu92017	E. coli P
875	48	100.0	20	9	ADJ02460	948	48	100.0	21	6	ABR62086	ABr62086	Anti-vitr
876	48	100.0	20	9	ADJ97505	949	48	100.0	21	6	ADA000850	ADa000850	Myc-His a
877	48	100.0	20	9	ADJ85434	950	48	100.0	21	6	ABU62470	ABu62470	N-terminu
878	48	100.0	20	9	ADJ21732	951	48	100.0	21	6	ABU62469	ABu62469	N-terminu
879	48	100.0	20	9	ADJ288431	952	48	100.0	21	6	ABU62468	ABu62468	N-terminu
880	48	100.0	20	9	AEJ00935	953	48	100.0	21	6	ABU62471	ABu62471	N-terminu
881	48	100.0	20	9	AEJ04240	954	48	100.0	21	6	ABU62467	ABu62467	N-terminu
882	48	100.0	20	9	AEJ44158	955	48	100.0	21	6	ABR63854	ABr63854	His tag P
883	48	100.0	20	9	AEJ10469	956	48	100.0	21	6	ADJ26386	ADj26386	CS198 pur
884	48	100.0	20	9	AEJ13165	957	48	100.0	21	7	ABU08854	ABu08854	Myc-His t
885	48	100.0	21	2	AAJ07063	958	48	100.0	21	7	ABR85348	ABr85348	Myc-His t
886	48	100.0	21	2	AAJ60142	959	48	100.0	21	7	AAE39150	AAe39150	Myc-His t
887	48	100.0	21	2	AAJ87745	960	48	100.0	21	7	ABW00603	ABw00603	Myc-His t
888	48	100.0	21	2	AAJ23653	961	48	100.0	21	7	ADG33993	ADg33993	Recombina
889	48	100.0	21	2	AAJ08590	962	48	100.0	21	7	ADG33984	ADg33984	L. intrac
890	48	100.0	21	2	AAJ23650	963	48	100.0	21	7	ADJ35718	ADj35718	Tyrosine
891	48	100.0	21	2	AAJ23647	964	48	100.0	21	7	ADJ66889	ADj66889	Lawsonia
892	48	100.0	21	2	AAJ5875	965	48	100.0	21	8	ADJ51136	ADj51136	Human PS2
893	48	100.0	21	2	AAJ54281	966	48	100.0	21	8	ADH41323	ADh41323	Recombina
894	48	100.0	21	2	AAJ48442	967	48	100.0	21	8	ADJ32465	ADj32465	Prostate
895	48	100.0	21	2	AAJ54435	968	48	100.0	21	8	ADJ51959	ADj51959	Repeat pr
896	48	100.0	21	2	AAJ79683	969	48	100.0	21	8	ADK51965	ADk51965	Repeat pr
897	48	100.0	21	2	AAJ97661	970	48	100.0	21	8	ADN17179	ADn17179	myc-His t
898	48	100.0	21	2	AAJ07403	971	48	100.0	21	8	ADN28580	ADn28580	myc-His P
899	48	100.0	21	2	AAJ08480	972	48	100.0	21	8	ADJ96647	ADj96647	Human PSI
900	48	100.0	21	2	AAJ05822	973	48	100.0	21	8	ADR46911	ADr46911	Myc-His P

```

974 48 100.0 21 8 ADR88369 Adt88369 pET15b ve
975 48 100.0 21 8 ADR70601 Adt70601 Histidine
976 48 100.0 21 8 ADR93231 Ob associ
977 48 100.0 21 9 ADV21143 myc-his t
978 48 100.0 21 9 ADM12411 Synthetic
979 48 100.0 21 9 ADM12414 Synthetic
980 48 100.0 21 9 ADM12413 Synthetic
981 48 100.0 21 9 ADM12410 Synthetic
982 48 100.0 21 9 ADM12412 Synthetic
983 48 100.0 21 9 ADM14189 MYC-HIS P
984 48 100.0 21 9 ADM71894 Myc-his t
985 48 100.0 21 9 ADM64710 Novel che
986 48 100.0 21 9 ADM18078 Peptide 1
987 48 100.0 21 9 ADX85499 Myc-His t
988 48 100.0 21 9 ADY50197 Vector PE
989 48 100.0 21 9 ADY59600 Myc-His t
990 48 100.0 21 9 ADY74021 Myc-his t
991 48 100.0 21 9 ADZ46753 pET15S co
992 48 100.0 21 9 ADZ69323 Mycobacte
993 48 100.0 21 9 ADZ67479 Mycobacte
994 48 100.0 21 9 AEA13722 Myc-His t
995 48 100.0 21 9 AEA21291 Nanoparti
996 48 100.0 21 9 AEB28815 Viral vec
997 48 100.0 21 9 AEB18116 PER405 L
998 48 100.0 21 9 AEB55205 myc-his t
999 48 100.0 21 9 AEB90810 Human Bcl1
1000 48 100.0 21 9 AEB72742 polh N-te

```

ALIGNMENTS

RESULT 1

AAy49221
ID AAY49221 standard; peptide; 6 AA.

AC AAY49221;

DT 07-FEB-2000 (first entry)

DE Nickel ion binding domain containing 6 His residues.

XX Monoclonal antibody; Mab; 1A7; GD2; immune response; melanoma;
KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
KW tumor-associated antigen.

XX Synthetic.

OS US5977316-A.

XX 02-NOV-1999.

PD 16-JAN-1996; 96US-00591196.

XX 17-JAN-1995; 95US-00372676.

XX (KENT) UNIV KENTUCKY.

XX Foon KA, Chatterjee SK, Chatterjee M;

XX WPI; 1996-354530/35.

PT Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s)
PT - useful to treat or palliate a GD2-associated disease, e.g. melanoma and
PT glioma.

XX Example 7; Col 58; 74pp; English.

CC The invention provides a monoclonal antibody (Mab) designated 1A7, which
CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
CC humans. Mab 1A7 has defined light and heavy chain variable region
CC sequences. The Mab 1A7 and polypeptides can be used for eliciting an anti
CC -GD2 immune response. The polypeptides can also be used for detecting or

CC purifying anti-GD2 antibody. The products can be used for treating GD2 -
CC associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue
CC carcinoma, and small cell carcinoma. They can be used for palliating the
CC disease or for reducing the risk of recurrence

SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 2

AAW19161
ID AAW19161 standard; peptide; 6 AA.

AC AAW19161;

DT 06-AUG-1997 (first entry)

DE Isoelectric point marker peptide 18.

KW Label; fluorescent dye; isoelectric; point; pI; marker; focusing;
KW fluorescence; capillary; stable.

XX Synthetic.

XX EP744614-A2.

XX 27-NOV-1996.

PD 29-MAR-1996; 96EP-00105113.

XX 31-MAR-1995; 95JP-00076873.

XX 19-OCT-1995; 95JP-00271196.

XX (MOLE-) LAB MOLECULAR BIOPHOTONICS.

XX Shimura K, Kasai K, Matsumoto H, Takamoto H;

XX WPI; 1997-001360/01.

PT Isoelectric point markers for isoelectric focusing - comprising
PT fluorescence-labelled oligo-nucleotide(s).

XX Claim 9; Page 21; 29pp; English.

CC The present peptide, when labelled with a fluorescent dye, can be used as
CC an isoelectric point (pI) marker for isoelectric focusing with
CC fluorescence. The dye is linked to the peptide's amino-terminal through
CC an amide, thioamide, sulphonamide, urea, thiourea or urethane bond, and
CC is rhodamine, fluorescein, cyanine, indocyanine, indocarbocyanine,
CC pyronine, lucifer yellow, quinacrine, squarillium, coumarin,
CC fluoranthranil maleimide or anthracene. The marker can be used for
CC capillary isoelectric focusing, and it is possible to construct peptide
CC sets that cover a wide pI range and have good storage stability. The
CC present peptide has respective observed and calculated pI values of 7.16
CC and 7.10

XX Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

```

RESULT 3
ID AAM18225 standard; peptide; 6 AA.
XX
AC AAM18225;
XX
DT 26-AUG-1997 (first entry)
XX
DE Purification tag of a TGF-beta fusion protein.
XX
KW Transforming growth factor-beta fusion protein; wound healing;
KM artificial skin; surgery recovery time.
XX
OS Synthetic.
XX
PN WO9639430-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US008973.
XX
PR 06-JUN-1995; 95US-00470837.
XX
PA (HALL/) HALL F L.
PA (NIMNI/) NIMNI M E.
PA (TUAN/) TUAN T.
PA (WU/L/) WU L.
PA (CHEU/) CHEUNG D T.
XX
PI Hall FL, Nimni ME, Tuan T, Wu L, Cheung DT;
XX
DR WPI: 1997-043065/04.
XX
DR N-PSDB: AAT71737.
XX
PT Prepn. of transforming growth factor-beta fusion protein - useful to
PT reduce surgery recovery time and to prepare artificial skin.
XX
PS Claim 5; Page 40; 59pp; English.
XX
CC A novel transforming growth factor-beta (TGF-beta) fusion protein
CC comprises a purification tag and a TGF active fragment. The present
CC sequence represents a specifically claimed purification tag.
CC Additionally, the fusion protein may comprise proteinase-sensitive linker
CC sites and binding domain so the protein sequence may contain some or all
CC of the following elements: purification tag;proteinase site;ECM binding
CC site;proteinase site:TGF-beta. TGF-beta promotes wound healing, and the
CC fusion protein can be used to reduce surgery recovery time and in the
CC preparation of artificial skin. The inclusion of a purification tag
CC facilitates purification of the fusion protein. The proteinase site is
CC included to permit cleavage and release of the purification tag after
CC purification if desired. The extracellular matrix binding site
CC facilitates delivery of the fusion protein to the desired site of action.
CC Delivery of the TGF-beta to the site to be treated reduces the amount of
CC TGF-beta required to be administered to be effective and reduces the
CC concentration of circulating TGF-beta which may result in undesirable
CC effects
CC
SQ Sequence 6 AA:
XX
Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHHHHH 6
DB 1 HHHHHH 6

```

```

AC AAM63024;
XX
DT 09-NOV-1998 (first entry)
XX
DE Hexa-histidine tag.
XX
KW Dectin-1; dendritic cell; c-type lectin; mouse; immunity; adjuvant;
KM allergy; autoimmune disease; gene therapy; vaccine; diagnosis;
XX drug screening; hexa-histidine tag.
XX
OS Synthetic.
XX
PN WO9828332-A2.
XX
PD 02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-US023761.
XX
PR 20-DEC-1996; 96US-00772440.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Arizumi K, Takashima A;
XX
DR WPI: 1998-377594/32.
XX
PT Nucleic acid encoding dendritic cell specific peptide(s) dectin-1 and -2
PT - useful, e.g. to regulate immune response, as vaccine adjuvants, for
PT diagnosis and drug screening.
XX
PS Claim 92; Page 157; 200pp; English.
XX
CC This hexa-histidine tag peptide is preferred for use in fusions with
CC murine dectin-1 (see AAM69236) or dectin-2 (see AAM69237) polypeptides of
CC the invention. The dectins are novel murine dendritic cell (DC) specific
CC members of the C-type lectin family that are essential for DC-mediated T
CC cell activation. The His-tagged polypeptides have been expressed in E.
CC coli host cells using recombinant vector pQE30, and used for production
CC of antibodies. The invention provides: dectin-1 and dectin-2 polypeptides
CC and DNA sequences, expression vectors, host cells, probes and primers,
CC antibodies, compounds that modulate dectin-mediated activation of T
CC cells, transgenic animals, and dectin ligands
CC
SQ Sequence 6 AA:
XX
Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHHHHH 6
DB 1 HHHHHH 6

```

```

RESULT 4
ID AAM63024 standard; peptide; 6 AA.
XX

```

```

RESULT 5
ID AAM69961 standard; peptide; 6 AA.
XX
AC AAM69961;
XX
DT 08-OCT-1998 (first entry)
XX
DE Poly-His tag for constructing soluble huRANKL.
XX
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KM immune response; inflammatory response; toxic shock; sepsis; TNF; RANKL;
KW RANK ligand; tumour necrosis factor.
XX
OS Synthetic.
XX
PN WO9828426-A2.
XX
PD 02-JUL-1998.

```

XX 22-DEC-1997; 97WO-US0233775.
 PF 23-DEC-1996; 96US-0059978P.
 XX 07-MAR-1997; 97US-00813509.
 PR 14-OCT-1997; 97US-0064671P.
 PA (IMNV) IMMUNEX CORP.
 PI Anderson DM, Galibert LJ, Maraskovsky E;
 XX WPI, 1998-377657/32.
 DR
 XX New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells.
 XX
 PS Example 15; Page 67; 80pp; English.
 XX
 CC This represents a poly-histidine tag used in the construction of a
 CC soluble huRANKL (RANK ligand). RANK (receptor activator of necrosis
 CC factor-kappaB (NF-kB) is a member of the tumour necrosis factor (TNF)
 CC family. A soluble RANK may be used for inhibiting activation of NF-kB by
 CC contacting a cell expressing membrane-associated RANK with a soluble RANK
 CC which binds to RANK ligand (RANKL). RANKL polypeptides can activate RANK
 CC and can be used to induce maturation of dendritic cells and enhance their
 CC allo-stimulatory capacity, thereby augmenting an immune response. The
 CC soluble RANK polypeptide composition may also be used for regulating an
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
 CC may be useful in ameliorating negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
 CC reactions. They can also be used in adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides
 CC can also be used to identify inhibitors of RANK and thus inhibitors of an
 CC inflammatory response, and also for protecting RANK-expressing cells
 CC from the negative effects of chemotherapy or the presence of high levels
 CC of TNF-alpha. The products can also be used for detection and drug
 CC screening
 CC
 XX Sequence 6 AA;
 SQ
 QY 1 HHHHHH 6
 DB 1 HHHHHH 6
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 6
 ID AAW68297 standard; peptide; 6 AA.
 XX AAW68297;
 AC
 XX
 DT 08-OCT-1998 (first entry)
 XX
 DE Poly-His tag for constructing soluble huRANKL.
 XX
 KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis; TNF; RANKL;
 KW RANK ligand; tumour necrosis factor.
 XX
 OS Synthetic.
 XX
 PN WO9828424-A2.
 XX
 PD 02-JUL-1998.
 XX
 PF 22-DEC-1997; 97WO-US023866.
 XX

PR 23-DEC-1996; 96US-0059978P.
 PR 07-MAR-1997; 97US-00813509.
 PR 14-OCT-1997; 97US-0064671P.
 PA (IMNV) IMMUNEX CORP.
 PI Anderson DM, Galibert LJ, Maraskovsky E;
 XX WPI, 1998-377655/32.
 DR
 XX New isolated receptor activator of necrosis factor-kappa B - useful for,
 PT e.g. developing products for regulating an immune or inflammatory
 PT response, treating toxic shock or sepsis.
 XX
 PS Example 15; Page 67; 80pp; English.
 XX
 CC This represents a poly-histidine tag used in the construction of a
 CC soluble huRANKL (RANK ligand). RANK (receptor activator of necrosis
 CC factor-kappaB (NF-kB) is a member of the tumour necrosis factor (TNF)
 CC family. Host cells transformed or transfected with an expression vector
 CC comprising the RANK encoding nucleic acid can be used to produce
 CC recombinant RANK protein. The soluble RANK may be used for inhibiting
 CC activation of NF-kB by contacting a cell expressing membrane-associated
 CC RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble
 CC RANK polypeptide composition may also be used for regulating an immune or
 CC inflammatory response. Inhibition of NF-kB by RANK antagonists may be
 CC useful in ameliorating negative effects of an inflammatory response that
 CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,
 CC graft-versus-host reactions, or acute inflammatory reactions. They can
 CC also be used in adjunct therapy for disease characterised by neoplastic
 CC cells that express RANK. The products can also be used for detection and
 CC drug screening
 CC
 XX Sequence 6 AA;
 SQ
 QY 1 HHHHHH 6
 DB 1 HHHHHH 6
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 7
 ID AAW44011 standard; peptide; 6 AA.
 XX AAW44011;
 AC
 XX
 DT 05-JUN-1998 (first entry)
 XX
 DE Poly-histidine peptide used in an epitope tagged prion protein construct.
 XX
 KW Prion; epitope; FLAG; Strep; poly-histidine; haemagglutinin; recombinant;
 KW transgenic animal; scrapie; Creutzfeldt-Jakob disease; CJD;
 KW bovine spongiform encephalopathy; BSE.
 XX
 OS Synthetic.
 XX
 PN WO9746572-A1.
 XX
 PD 11-DEC-1997.
 XX
 PF 29-MAY-1997; 97WO-US009289.
 XX
 PR 06-JUN-1996; 96US-00660626.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Prusiner SB, Telling GC, Cohen FE, Scott MR;
 XX WPI, 1998-042112/04.
 DR

XX Nucleic acid construct encoding biologically active protein and epitope -
 PT especially epitope-tagged prion protein.
 XX
 PS Claim 4; Page 48; 62pp; English.
 CC This is the sequence of an artificial poly-histidine peptide epitope. It
 CC is used in a recombinant nucleic acid construct encoding an epitope-
 CC tagged prion protein (PrP). The construct comprises a first nucleic acid
 CC sequence encoding a biologically active protein
 CC fragment and a second nucleic acid sequence encoding a heterologous
 CC epitope domain. The heterologous epitope domain is a peptide selected
 CC from a peptide group of FLAG, Strept, poly-histidine, human c-myc peptide
 CC recognised by monoclonal antibody 9B10 and haemagglutinin peptide
 CC recognised by monoclonal antibody 12CA5. The protein is a natural,
 CC synthetic or chimeric PrP molecule. The protein has two different three-
 CC dimensional conformations and the epitope domain is spatially positioned
 CC relative to the protein such that the epitope domain is more exposed in a
 CC first conformation relative to a second conformation. The nucleic acid
 CC construct may be used for the production of transgenic animals or cells
 CC that are useful in a method for distinguishing between different
 CC conformational shapes of a protein. These methods are particularly useful
 CC in studying diseases caused by prion proteins, e.g. Creutzfeldt-Jakob
 CC disease (CJD), scrapie and bovine spongiform encephalopathy (BSE).
 CC
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HHHHHH 6
 Db 1 HHHHHH 6
 RESULT 8
 ID AAE08742
 ID AAE08742 standard; peptide; 6 AA.
 AC AAE08742;
 DT 15-NOV-2001 (first entry)
 XX
 DE Poly-His tag, to generate soluble RANKL.
 XX Receptor activator of nuclear factor kappa B ligand; RANKL; NF;
 KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
 KW immune response; inflammatory response; graft-versus-host reaction;
 KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
 KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.
 XX
 OS Synthetic.
 XX
 XX US6271349-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 17-DEC-1998; 98US-00215649.
 XX
 XX 23-DEC-1996; 96US-0059978P.
 PR 23-DEC-1996; 96US-00772330.
 PR 07-MAR-1997; 97US-0077181P.
 PR 07-MAR-1997; 97US-00813509.
 PR 14-OCT-1997; 97US-0064671P.
 PR 22-DEC-1997; 97US-00996139.
 XX
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 XX Dougall WC, Galibert L;
 XX
 DR WPI; 1998-377655/32.
 XX

PT New isolated receptor activator of necrosis factor-kappa B - useful for,
 PT e.g. developing products for regulating an immune or inflammatory
 PT response, treating toxic shock or sepsis.
 XX
 PS Example 15; Col 81; 47pp; English.
 CC
 CC The patent discloses novel receptor activator of nuclear factor (NF) -
 CC kappa B (RANK) proteins and their corresponding DNAs. RANK is a member of
 CC the tumour necrosis factor (TNF) receptor superfamily and associates with
 CC TNF receptor associated factor (TRAF) 2 and 3 which are important in the
 CC regulation of immune and inflammatory response. The receptors are useful
 CC for regulating immune response and in screening for inhibitors of these
 CC receptors. The cytoplasmic domain of RANK is used in developing assays
 CC for inhibitors of signal transduction, e.g. for screening the molecules
 CC that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and
 CC particularly TRAF6. NF-kappa B inhibition by RANK antagonists are useful
 CC in ameliorating the negative effects of an inflammatory response that
 CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,
 CC graft-versus-host reactions, acute inflammatory reactions and the effects
 CC of bone resorption. RANK acts as an anti-apoptotic signal and rescue the
 CC cells that express RANK from apoptosis. Soluble forms of the receptor are
 CC used in vivo or in vitro based screening tests for agonists or
 CC antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B
 CC activation, or to inhibit transduction of a signal via RANK.
 CC Compositions are used in the development of both agonistic and
 CC antagonistic antibodies, or as an adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. Compounds that
 CC interfere with RANK/TRAF6 interactions are useful for modulating the
 CC formation of osteoclasts from osteoclast precursors and for modulating
 CC osteoclast function and activities. They are used as inhibitors of
 CC diseases associated with excess bone resorption and as immunosuppressants
 CC or anti-inflammatory agents. The RANK DNAs are useful for the expression
 CC of recombinant proteins, as probes for analysis of the presence or
 CC distribution of RANK transcripts, while the proteins are useful in
 CC preparing kits for the detection of soluble RANK, or monitor RANK-related
 CC activity. The present sequence is a poly-His tag which is used in the
 CC exemplification of the invention to generate a soluble, tagged, poly-His
 CC version of human and murine RANKL.
 CC
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HHHHHH 6
 Db 1 HHHHHH 6
 RESULT 9
 ID ADV42333
 ID ADV42333 standard; peptide; 6 AA.
 AC ADV42333;
 DT 10-FEB-2005 (first entry)
 XX
 DE Hexahistidine tag used to facilitate D(II) FGFR1 purification.
 XX
 KW Protein stabilization; protein renaturation; drug screening;
 KW high throughput screening; protein purification; protein folding.
 XX
 OS Synthetic.
 XX
 XX WO9742500-A1.
 XX
 PD 13-NOV-1997.
 XX
 PF 09-MAY-1997; 97WO-US008154.
 XX
 PR 09-MAY-1996; 96US-0017860P.
 XX

PA (THRE-) 3-DIMENSIONAL PHARM INC.
 XX Pantoliano MW, Rhind AW, Salemm FR, Springer BA, Bone RF;
 PI Petrella EC;
 XX WPI; 1998-008452/01.
 DR
 XX
 XX Ranking efficiency of molecules and conditions for stabilising target
 PT molecule - from their effect on thermal denaturation curves, particularly
 PT for identifying agents that favour refolding or crystallisation of
 PT proteins and for assessing affinity for target receptors.
 XX
 PS Example 19, Fig 27, 176pp, English.
 XX
 XX The invention relates to a multi-variable method for ranking the
 CC efficiency of different molecules (e.g., a protein or nucleic acid) which can
 CC stabilizing a target molecule (e.g., a protein or nucleic acid) which can
 CC be denatured by heat. The method comprises: (a) treating a target
 CC molecule, in separate containers, with various different molecules or
 CC biochemical conditions; (b) heating the containers simultaneously and
 CC measuring a physical change associated with denaturation of the target
 CC molecule; (c) generating a thermal denaturation curve for each container;
 CC (d) comparing these curves with each other and with a reference curve
 CC obtained under specified conditions; and (e) ranking efficiency according
 CC to changes in each curve. The invention also relates to a device
 CC comprising many containers in a carrier, each container containing a
 CC different candidate stabilisation molecule plus one molecule from a
 CC combinatorial library; and apparatus that can simultaneously heat many
 CC samples (particularly according to a predetermined temperature profile)
 CC and receive spectral emissions from the samples. The method of the
 CC invention can additionally be adapted to assess molecules and conditions
 CC that facilitate refolding of a denatured protein or crystallization of a
 CC protein; to rank affinity of a molecule for a particular target molecule;
 CC and to rank different molecules or biochemical conditions for optimal
 CC shelf life of proteins. The method of the invention may be specifically
 CC applied to proteins and nucleic acids, particularly where they are
 CC members of combinatorial libraries. In particular, the method can be used
 CC to identify optimum conditions for renaturing recombinantly produced
 CC proteins present in inclusion bodies, or to identify lead compounds from
 CC their high affinity for a selected receptor. The simultaneous heating of
 CC many samples ensures rapid, high throughput screening and the method
 CC provides quantitative information. It can measure binding affinities in
 CC the range 0.1 nM to 0.001 pM in a single well, does not require
 CC radioactive labels, is applicable to any receptor that is a drug target,
 CC and requires only very small (e.g., 5-40 pmole) samples. The new
 CC apparatus provides both heat control and spectral measurements,
 CC eliminating the need for transfers between instruments. The present
 CC sequence represents a hexahistidine tag present in the N-terminus of a
 CC recombinantly produced D(II) domain of fibronectin growth factor receptor
 CC 1 (FGFR1) and used to facilitate purification. The D(II) FGFR1 protein
 CC was used to screen biochemical conditions that facilitate protein folding
 CC in an example of the invention.
 CC
 XX Sequence 6 AA:
 SQ
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 DB 1 HHHHHH 6
 RESULT 10
 AA06469
 ID AA06469 standard; peptide; 6 AA.
 XX
 XX AA06469;
 AC
 XX
 XX 27-SEP-1999 (first entry)
 DT
 XX
 DE Epitope tag.

XX
 XX Epitope tag; antibody engineering; yeast; surface display;
 KM protein library; peptide library.
 XX
 XX Synthetic.
 OS
 XX WO9336569-A1.
 XX
 XX
 XX 22-JUL-1999.
 PD
 XX
 XX 20-JAN-1999; 99WO-US001188.
 PF
 XX
 XX 20-JAN-1998; 98US-00009388.
 PR
 XX 26-AUG-1998; 98US-00140084.
 XX
 XX (UNIT I) UNIV ILLINOIS FOUND.
 PA
 XX
 XX Wittrup KD, Kieke MC, Kranz DM, Shuster E, Boder ET;
 PI WPI; 1999-430619/36.
 DR
 XX
 XX
 XX This peptide comprises an epitope tag that can be used in methods of the
 CC invention. The invention discloses a powerful new system for engineering
 CC antibody affinity and specificity, by constructing a microbial analogue
 CC of the mammalian system's B cell repertoire. Antibodies are displayed on
 CC the surface of yeast cells by genetic fusion with yeast cell wall
 CC proteins, especially agglutinin proteins. After mutation, variants are
 CC selected on the basis of improved binding characteristics with
 CC fluorescently labeled targets. The selection method also identifies
 CC proteins with enhanced phenotypic characteristics, proteins that are
 CC displayed at higher levels, proteins that are secreted at higher
 CC efficiency and proteins of improved stability
 CC
 XX Sequence 6 AA:
 SQ
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 DB 1 HHHHHH 6
 RESULT 11
 AA064203
 ID AA064203 standard; peptide; 6 AA.
 XX
 XX AA064203;
 AC
 XX
 XX 25-MAR-1999 (first entry)
 DT
 XX
 XX Peptide comprising a purification tag.
 DE
 XX
 XX Proteinase site; bone morphogenetic fusion protein; bone binding site;
 KM bone morphogenetic protein; transforming growth factor beta;
 KW active fragment; wound healing; bone growth; purification tag.
 XX
 XX Synthetic.
 OS
 XX WO9855137-A1.
 XX
 XX 10-DEC-1998.
 PD
 XX
 XX 02-JUN-1998; 98WO-US011189.
 PF
 XX
 XX 03-JUN-1997; 97US-00868452.
 PR
 XX

PA (NIMN/) NIMNI M E.
 PA (HALL/) HALL F L.
 PA (WILL/) WU L.
 PA (HAMB/) HAN B.
 PA (SHOR/) SHORS E C.
 XX
 PI Nimni ME, Hall FL, Wu L, Han B, Shors EC,
 DR WPI, 1999-059875/05.
 DR N-PSDB; AAV99371.
 XX
 PT New bone morphogenetic fusion proteins - comprising a purification tag
 PT and a bone morphogenetic active fragment, used for enhancing wound
 PT healing or bone growth.
 XX
 PS Claim 5, Page 38; 64pp; English.
 CC
 CC The present sequence represents a peptide comprising a purification tag
 CC that was used in the creation of the bone morphogenetic fusion proteins
 CC of the invention. The bone morphogenetic fusion protein may contain some
 CC or all of the following elements: a purification tag, a proteinase site,
 CC an ECM/bone binding site, a second proteinase site, and a bone
 CC morphogenetic protein active fragment. The fusion proteins of the
 CC invention also includes proteins that have transforming growth factor
 CC beta active fragments instead of bone morphogenetic protein active
 CC fragments. The bone morphogenetic fusion proteins can be used for
 CC enhancing wound healing or bone growth
 CC
 SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 1 HHHHHH 6

RESULT 12
 AAY17447
 ID AAY17447 standard; peptide; 6 AA.
 XX
 AC AAY17447;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Major outer membrane protein amino terminal peptide #5.
 XX
 KW Major outer membrane protein; MOMP; Chlamydia trachomatis; antibody;
 KW antigen.
 XX
 OS Synthetic.
 OS
 PN JP1123078-A.
 PN
 PD 11-MAY-1999.
 PD
 PF 22-OCT-1997; 97JP-00289938.
 PF
 PR 22-OCT-1997; 97JP-00289938.
 PR
 PA (ELED) DENKI KAGAKU KOGYO KK.
 PA
 XX WPI, 1999-340514/29.
 DR
 XX
 PT New major outer membrane protein of Chlamydia trachomatis - useful for
 PT determination of Chlamydia trachomatis antibody.
 XX
 PS Claim 2; Page 7; 11pp; Japanese.
 CC
 CC The present invention describes a major outer membrane protein (MOMP) of
 CC Chlamydia trachomatis in which six amino acid residues are peptide-bound

CC to the amino terminal and which has immunological activity. Also
 CC described are: (1) a method for the preparation of MOMP of Chlamydia
 CC trachomatis in which the gene of the above MOMP of Chlamydia trachomatis
 CC is inserted to an expression vector used to transform E. coli, the
 CC transformant is cultured under conditions where the MOMP of Chlamydia
 CC trachomatis is expressed and the expression product is collected from the
 CC transformant; (2) a method for the determination of the antibody of MOMP
 CC of Chlamydia trachomatis using the above MOMP of Chlamydia trachomatis as
 CC the antigen; and (3) a reagent for the determination of the antibody of
 CC MOMP of Chlamydia trachomatis using the above major MOMP of Chlamydia
 CC trachomatis as the antigen. The method can provide an antigen used for
 CC the determination of Chlamydia trachomatis antibody
 CC
 SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 1 HHHHHH 6

RESULT 13
 AAY09544
 ID AAY09544 standard; peptide; 6 AA.
 XX
 AC AAY09544;
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DE Human TAK1 6xHis peptide.
 XX
 KW Human, TAK1; screening; inhibition; TGF-beta;
 KW transforming growth factor beta.
 XX
 OS Homo sapiens.
 OS
 PN WO9921010-A1.
 PN
 PD 29-APR-1999.
 PD
 PF 22-OCT-1998; 98WO-JP004796.
 PF
 PR 22-OCT-1997; 97JP-00290188.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX
 PA Ono K, Ohtomo T, Tsuchiya M;
 PI
 PI WPI, 1999-312645/26.
 DR
 XX
 PT Screening for TGF-beta inhibitory substances, which are useful as drugs
 PT for treatment of diseases relating to its disorder.
 XX
 PS Example 1; Page 58; 195pp; Japanese.
 CC
 CC A method has been developed for screening for substances which inhibit
 CC the binding of TAK1 polypeptide to TAK1 polypeptide. The method
 CC comprises: (a) contacting the polypeptide in the presence of a sample;
 CC and (b) detecting the amount of bound polypeptide, in which the sample
 CC can be pre-mixed with TAK1 or TAK1 polypeptide first. The transforming
 CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
 CC indications e.g. as TGF-beta signal transduction inhibitors or
 CC activators, or extracellular matrix protein production enhancement
 CC inhibitors or activators, or cell proliferation prevention inhibitors or
 CC activators, or monocyte migration inhibitors or activators, or
 CC physiological activity induction inhibitors or activators, or
 CC immunosuppression inhibitors or activators, or amyloid beta protein
 CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence represents a peptide from an example of

CC the present invention
XX Sequence 6 AA;
SQ

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 14
AA33592
ID AA33592 standard; protein; 6 AA.

AC AA33592;
DT 20-DEC-1999 (first entry)
XX
XX

DE VH-VL domain linker peptide #4.

XX Antigen binding; single chain; variable domain; VH domain; light chain;
XX heavy immunoglobulin chain; VL domain; anticancer; antiviral; tumor;
XX antibacterial; antimetastatic; antiinflammatory; treatment; prevention;
XX diagnosis; vaccine; autoimmune disease; inflammation; blood disorder;
XX transplant rejection; arthritis; nervous system disorder; infection.

OS Synthetic.

PN DE19816141-A1.

PD 14-OCT-1999.

XX 09-APR-1998; 98DE-01016141.

PR 09-APR-1998; 98DE-01016141.

XX (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

PI Kontermann R, Sedlacek H, Mueller R;

DR WPI; 1999-581511/50.

XX New polypeptide binding agents containing variable heavy and light
XX constructs connected via peptide linker, used for treatment, prevention
XX or diagnosis of e.g. cancer.

PS Example 1; Page 15; 20pp; German.

XX This sequence represents a novel single-chain molecule (I) that binds
XX multiple antigens and comprises two variable domains of heavy
XX immunoglobulin chains (VH), having specificities A and B and two variable
XX domains of light chains (VL), also with specificities A and B. The
XX domains are provided as two VH-VL constructs which are attached via a
XX peptide (P). Any VH and VL may be replaced by their functional fragments.
XX The products of the invention have anticancer, antiviral, antibacterial,
XX antimetastatic and antiinflammatory activity. (I) are used to treat,
XX prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases
XX and inflammation (e.g. transplant rejection and arthritis), blood
XX disorders (e.g. of the coagulation and/or circulatory systems, such as
XX anemia, leucopenia, thrombocytopenia and hypertension), nervous system
XX disorders and/or infections (by viruses or bacteria, or malaria),
XX including, when (I) include a fusogenic peptide, use for gene transfer.
XX (I) are produced simply and in predominantly homogeneous form, in a wide
XX variety of hosts, either in secreted or membrane-bound forms. This
XX sequence represents a VH-VL domain linker peptide which is used to
XX illustrate the method of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 15
AAE1561
ID AAE1561 standard; peptide; 6 AA.

AC AAE1561;

DT 09-APR-2002 (first entry)

DE Epitope tag #5 fused to yeast cell wall protein AGA2.

XX Yeast cell wall protein; AGA2; T cell receptor; multiple sclerosis;
XX cancer; sepsis; autoimmune disease; arthritis; diabetes.

OS Synthetic.

PN US6331391-B1.

PD 18-DEC-2001.

XX 20-JAN-1998; 98US-00009388.

PR 31-MAY-1996; 96US-0018741P.

PR 30-MAY-1997; 97US-00866398.

XX (UNII) UNIV ILLINOIS FOUND.

PI Witterup KD, Kranz DM, Kleke M, Boder ET;

DR WPI; 1999-430619/36.

XX Selecting proteins with enhanced phenotypic properties than wild-type
XX proteins, is useful for highly specific cancer diagnosis and therapy.

PS Claim 40; Col 60; 59pp; English.

XX The present invention relates to a method for selecting proteins for
XX displayability on a yeast cell surface. The method comprises transforming
XX yeast cells with a vector that expresses a test protein fused to a yeast
XX cell wall protein (AGA2), contacting the cells with a label that binds to
XX proteins displayed on the cell wall, and isolating label-bound cells,
XX where the test protein is from a variegated population generated by
XX engineering. The invention is also directed to new processes for
XX engineering T cell receptor for improved binding properties. Improved T
XX cell receptor molecules are useful in therapies for cancer, sepsis,
XX autoimmune diseases such as arthritis, diabetes or multiple sclerosis.
XX The methods are useful to select proteins with altered affinity, altered
XX specificity or conditional binding. The present sequence is an epitope
XX tag fused between protein of interest and yeast cell wall protein AGA2

SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 16
AA50711
ID AA50711 standard; peptide; 6 AA.

XX AA50711;

XX 20-MAR-2003 (revised)
 DT 08-FEB-2000 (first entry)
 XX
 DE Single chain antibody construct polystyridine tag.
 XX
 KW Immunoglobulin; light chain; VL region; heavy chain; VH region;
 KW single-chain; antigen binding; variable domain; anticancer; treatment;
 KW antiviral; antibacterial; antimalarial; antiinflammatory; diagnosis;
 KW tumor vaccine; autoimmune disease; inflammation; blood disorder;
 KW nervous system; infection.
 XX
 OS Unidentified.
 XX
 PN DE19827239-A1.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1998; 98DE-01027239.
 XX
 PR 09-APR-1998; 98DE-01016141.
 PR 18-JUN-1998; 98DE-01027239.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 XX
 PI Kontermann R, Sedlacek H, Mueller R;
 XX
 DR WPI; 1999-591691/51.
 XX
 PT New polyspecific binding agents useful for treatment, prevention and
 PT diagnosis of cancer and autoimmune diseases comprises variable domains of
 PT heavy and light chains of immunoglobulins bound by a peptide.
 XX
 PS Example 1; Page 17; 26pp; German.
 XX
 CC This invention describes a novel single-chain molecule (I) that binds
 CC multiple antigens and comprises two variable domains of heavy
 CC immunoglobulin chains (VH) and two variable domains of light chains (VL).
 CC The domains are provided as two VH-VL constructs which are attached via a
 CC peptide (P). Any VH and VL may be replaced by their functional fragments.
 CC The products of the invention have anticancer, antiviral, antibacterial,
 CC antimalarial, and antiinflammatory activity. (I) are used to treat,
 CC prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases
 CC and inflammation (e.g. transplant rejection and arthritis), blood
 CC disorders (e.g. of the coagulation and/or circulatory systems, such as
 CC anemia, leucopenia, thrombocytopenia and hyperension), nervous system
 CC disorders and/or infections (by viruses or bacteria, or malaria),
 CC including, when (I) include a fusogenic peptide, use for gene transfer.
 CC This sequence represents a polystyridine tag which is used in the
 CC construction of the single chain construct described in the invention.
 CC NOTE: This specification is a treat as basic for C2-9901215 in Derwent
 CC week 9951. (Updated on 20-MAR-2003 to correct DR field.)
 CC
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 |||||
 DB 1 HHHHHH 6
 RESULT 17
 AAY78351
 ID AAY78351 standard; peptide; 6 AA.
 XX
 AC AAY78351;
 XX
 DT 05-MAY-2000 (first entry)
 XX
 DE His-6 peptide SEQ ID NO:2.

XX Caspase; protein array; screening; biomolecular activity; proteomic;
 KW drug development; biosensor; diagnosis.
 KW
 OS Synthetic.
 XX
 PN WO200004382-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 14-JUL-1999; 99WO-US015971.
 XX
 PR 14-JUL-1998; 98US-00115455.
 XX
 PA (ZYOM-) ZYOMTX INC.
 XX
 PI Wagner P, Ault-Riche D, Nock S, Itin C;
 XX
 DR WPI; 2000-171289/15.
 XX
 PT New arrays for analyzing components of a fluid sample, useful for drug
 PT development, functional proteomics, clinical diagnostics and biosensors.
 XX
 PS Example 9; Page 58; 81pp; English.
 XX
 CC The present invention describes an array (I) of proteins comprising a
 CC substrate, at least one organic thinfilm on some or all of the substrate
 CC surface, and patches arranged in discrete, known regions on portions of
 CC the substrate surface covered by organic thinfilm. Each of the patches
 CC comprises a protein immobilised on the underlying organic thinfilm. The
 CC arrays can be used for screening proteins for their ability to interact
 CC with a component of a sample. They can also be used for assaying for
 CC protein-protein binding interactions or analyses. They can be used for
 CC drug development, proteomics, clinical diagnostics and biosensors. The
 CC present sequence represents a peptide used in the exemplification of the
 CC present invention
 CC
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 48; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 |||||
 DB 1 HHHHHH 6
 RESULT 18
 AAY99641
 ID AAY99641 standard; peptide; 6 AA.
 XX
 AC AAY99641;
 XX
 DT 27-OCT-2000 (first entry)
 XX
 DE His6 tag used to create pDANS D1.3 phagemid.
 XX
 KW His6 tag; gene library production.
 KW
 OS Synthetic.
 XX
 PN WO200031246-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 18-NOV-1999; 99WO-EP008856.
 XX
 PR 19-NOV-1998; 98IT-MI002509.
 XX
 PA (SISS-) SISSA SCUOLA INT SUPERIORE DI STUDI AVAN.
 XX
 PI Bradbury ARM, Sblattero D;

```

XX      WPI; 2000-400060/34.
XX
XX      Preparation of highly diverse nucleic acid and polypeptide libraries.
PT      Useful for the derivation of polypeptides with useful characteristics.
XX
XX      Example 2; Page 75; 76pp; English.
XX
XX      The present sequence is a His6 tag. It was used in the creation of a
CC      phagemid which, when transfected into a bacterial cell, was able to
CC      recombine with similar phagemids. This is useful for producing DNA
CC      libraries, as previous libraries have contained sequences which it is not
CC      possible to recombine further, they contained many contaminating
CC      sequences, and did not allow recombination between plasmids. This library
CC      overcomes these problems and allows the creation of large and highly
CC      diverse libraries
XX
SQ      Sequence 6 AA;

Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
        1 HHHHHH 6

Db
1 HHHHHH 6

RESULT 19
ABB08438
ID      ABB08438 standard; peptide; 6 AA.
XX
XX      ABB08438;
XX
XX      07-MAY-2002 (first entry)
XX
XX      Histidine tag relative to the farnesyltransferase of the invention.
XX
XX      Farnesyltransferase; enzyme.
XX
XX      Unidentified.
XX
XX      KR98075770-A.
XX
XX      16-NOV-1998.
XX
XX      01-APR-1997; 97KR-00012067.
XX
XX      01-APR-1997; 97KR-00012067.
XX
XX      01-APR-1997; 97KR-00012067.
XX
XX      (GLDS ) LG CHEM LTD.
XX
XX      Moon GD, Kim MJ, Chung HH;
XX
XX      WPI; 2000-020309/02.
XX
XX      N-PSDB; ABA98900.
XX
XX      Farnesyltransferase having histidine tag and process for preparing the
PT      same.
XX
XX      Disclosure; Page 23; 23pp; Korean.
XX
XX      The invention relates to a farnesyltransferase with a histidine tag, and
CC      methods for preparing it. The current sequence represents a histidine tag
CC      relative to the farnesyltransferase of the invention
XX
XX      Sequence 6 AA;

Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6

```

```

Db      1 HHHHHH 6

RESULT 20
AAV78346
ID      AAV78346 standard; peptide; 6 AA.
XX
XX      AAV78346;
XX
XX      05-MAY-2000 (first entry)
XX
XX      His-6 peptide SEQ ID NO:2.
XX
XX      Immunoglobulin; protein capture; detection; antibody; proteomic;
XX      drug screening; diagnosis.
XX
XX      Synthetic.
XX
XX      WO200004389-A2.
XX
XX      27-JAN-2000.
XX
XX      14-JUL-1999; 99WO-US015968.
XX
XX      14-JUL-1998; 98US-00115455.
XX
XX      (ZYOM-) ZYOMYX INC.
XX
XX      Wagner P, Nock S, Ault-Riche D, Itin C;
XX
XX      WPI; 2000-161175/14.
XX
XX      New arrays for assaying proteins, used for analysis of cell expression
PT      products, evaluating disease conditions, proteomics, drug screening,
PT      diagnostics and measurement of gene activity.
XX
XX      Example 6; Page 68; 90pp; English.
XX
XX      The present invention describes an array of protein-capture agents (PCA),
CC      comprising a substrate, at least one organic thinfilm covering some or
CC      all of the surface of the substrate, and patches arranged in discrete,
CC      known regions on the portions of the substrate surface covered by organic
CC      thinfilm. Each patch comprises PCAs, capable of binding a particular
CC      expression product, or a fragment of a cell population, immobilised on
CC      the organic thinfilm. The array comprises different PCAs, capable of
CC      binding different expression products, or fragments, of the cell
CC      population. The arrays can be used for assaying for expression products
CC      or fragments of a cell or population of cells. They can be used for
CC      evaluating a disease condition in a tissue of an organism. They can be
CC      used in proteomics, drug screening, diagnostics, and the measurement of
CC      gene activity at the protein level in cells. The present sequence
CC      represents a peptide used in an example from the present invention
XX
XX      Sequence 6 AA;

Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
        1 HHHHHH 6

Db
1 HHHHHH 6

RESULT 21
AAV77706
ID      AAV77706 standard; peptide; 6 AA.
XX
XX      AAV77706;
XX
XX      12-MAY-2000 (first entry)
XX

```

DE 6-His peptide epitope.
 XX Cell surface receptor; luminescence; protein internalization;
 KM drug discovery; screening assay; epitope.
 XX Synthetic.
 OS
 PN WO20003246-A2.
 XX
 PD 20-JAN-2000.
 XX
 PE 13-JUL-1999; 99WO-US015870.
 XX
 PR 13-JUL-1998; 98US-0092671P.
 XX
 PA (CELL-) CELLOMICS INC.
 XX
 PI Rubin RA, Giuliano KA, Gough A, Dunlay T;
 XX WPI; 2000-171170/15.
 DR
 PT Automated screening method for identifying compounds which induce cell
 PT surface receptor internalization, useful for drug discovery.
 PS
 SQ Example 6; Page 67; 148pp; English.
 XX
 CC The invention relates to a method for identifying compounds which inhibit
 CC internalization of cell surface receptors. Provided are an array of
 CC locations, each containing cells with a cell surface receptor protein,
 CC that are treated with a test compound. The protein is luminescently
 CC labeled or contacted with a luminescently labeled cell before or after
 CC test compound treatment. Any luminescence produced is converted into
 CC digital data and automatically analysed to determine if the test compound
 CC induced the protein internalization. The novel method is used to screen
 CC for compounds which modulate cell surface receptor protein
 CC internalization, this can be used in drug discovery, to test compound
 CC efficacy in living biological systems. The assay method is automated and
 CC compact. It has high throughput and uses smaller volumes of reagents and
 CC test compounds. Sequences AAY7704-718 represent examples of peptide
 CC epitope tags used in the course of the invention
 CC
 SQ Sequence 6 AA;
 XX
 QY
 Db 1 HHHHHH 6
 1 HHHHHH 6
 1 HHHHHH 6

Query Match 100.0%; Score 48; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;

RESULT 22
 AAY96951
 ID AAY96951 standard; peptide; 6 AA.
 XX
 AC AAY96951;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Polyhistidine tag for use in rubredoxin fusion protein.
 XX
 KM PRUBEX; polyhistidine; tag; rubredoxin; antigen; vaccine; carrier;
 KM immunogenic; flag tag; fusion.
 XX
 OS Synthetic.
 XX
 PN WO200039310-A1.
 XX
 PD 06-JUL-2000.
 XX
 PE 29-DEC-1999; 99WO-US031176.
 XX

PR 29-DEC-1998; 98US-00114034.
 XX
 XX (UNGE-) UNIV GEORGIA RES FOUND INC.
 PA Przybyla A, Menon N;
 PI
 XX WPI; 2000-452403/39.
 DR
 XX
 PT Nucleic acids encoding fusion peptides comprising rubredoxin, useful as
 PT vaccines.
 PS
 PS Claim 16; Page 61; 67pp; English.
 XX
 CC Fused proteins comprising rubredoxin and fused antigens and/or happens
 CC may be used as vaccines to initiate immune responses. In this case, the
 CC rubredoxin acts as a carrier. The fusion protein is capable of binding
 CC iron (Fe-2+) when properly folded, giving it a red color that makes it
 CC easy to identify following or during purification. The C-terminal fused
 CC protein may be insoluble or known to form inclusion bodies in a host
 CC cell. The rubredoxin serves as the carrier molecule to yield immunogenic
 CC fusion products. As rubredoxin is itself only negligibly antigenic, there
 CC is no need to include a cleavage site in the fusion product to allow
 CC cleavage of the N-terminal and C-terminal constituents
 CC
 SQ Sequence 6 AA;
 XX
 QY
 Db 1 HHHHHH 6
 1 HHHHHH 6
 1 HHHHHH 6

Query Match 100.0%; Score 48; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;

RESULT 23
 AAB10788
 ID AAB10788 standard; peptide; 6 AA.
 XX
 AC AAB10788;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE B. subtilis lumazine synthase protein fragment #15.
 XX
 KM Lumazine synthase; capsid; cytosolic; antiviral; antibacterial; vaccine;
 KM gene therapy; immunotherapy; biosensor; diagnosis.
 XX
 OS Bacillus subtilis.
 XX
 PN WO200053229-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 03-MAR-2000; 2000WO-EP001899.
 XX
 PR 08-MAR-1999; 99DE-01010102.
 XX
 PA (FISC/) FISCHER M.
 PA (BACH/) BACHER A.
 XX
 PI Fischer M, Bacher A;
 XX WPI; 2000-572230/53.
 DR
 XX Protein conjugate based on lumazine synthase as carrier, useful e.g. for
 XX vaccination and immunotherapy, contains many functional molecules
 XX attached to outside of the carrier.
 PT
 PS Claim 43b; Page 100; 180pp; German.
 XX
 CC This invention describes a novel protein conjugate (1) comprising at
 CC least 1 functional region (FR) at any position in the sequence of a

CC carrier protein (II) to form a capsid three-dimensional structure of the
 CC lumazine synthase (LS) type, such that the outer periphery is covalently
 CC linked to many FR. The invention also describes (1) a hetero-oligomeric
 CC protein conjugate (Ia) comprising either a mixture of at least 2
 CC different (I) or of at least 1 (I) and at least 1 (II) that lacks FR,
 CC with the components optionally covalently linked by chemical treatment;
 CC (2) a method for preparation of (I) and (Ia); (3) a vector for
 CC preparation of (I); (4) a DNA (III) that encodes (I); (5) LS from
 CC *Bacillus subtilis* with Cys 93 and/or Cys139 replaced by Ser; (6) DNA
 CC (IIa) encoding LS from *Aquifex aeolicus* which is codon-optimized for
 CC expression in a recombinant *Escherichia coli* strain; (7) a chimeric
 CC protein (CP) comprising amino acids (aa) 1-60 from LS of *B. subtilis* and
 CC aa 61-154 from LS of *A. aeolicus* for use as (II); and (8) pharmaceutical
 CC compositions and vaccines containing (I) and (Ia). The products of the
 CC invention have cytotoxic, antiviral and antibacterial activity and can
 CC be used in a vaccine or for gene therapy. (I) are used as pharmaceuticals
 CC (e.g. for immunotherapy of human immune deficiency virus infection or
 CC tumors) and in vaccines, including multivalent vaccines, against
 CC bacterial or viral infections, to produce diagnostic or therapeutic
 CC antibodies, for selective detection, purification and characterization of
 CC antibodies, and for preparation of protein libraries. (I) may also be
 CC used as biosensors and for diagnosis, e.g. of tumors. Genes that encode
 CC (I) are useful in DNA vaccines and for preparation of plant-based oral
 CC vaccines. (I) can contain many FR (same or different) at the surface of a
 CC spherical particle (LS comprises 60 subunits that assemble into an
 CC icosahedron). The large number of FR may increase sensitivity in
 CC immunoassays and the efficiency of immunotherapy agents

XX Sequence 6 AA:
 SQ

Query Match 100.0%; Score 48; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHHHHH 6
 1 HHHHHH 6

Db

RESULT 24
 AAB59857
 ID AAB59857 standard; peptide; 6 AA.

XX AAB59857;

XX 30-MAR-2001 (first entry)

XX 6-His peptide epitope.

XX 6-His peptide epitope; macromolecule trafficking; endosomal system;

XX membrane receptor internalisation.

XX Unidentified.

XX WO200079241-A2.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-US040260.

XX 21-JUN-1999; 99US-0140143P.

XX 12-JUL-1999; 99US-00352171.

XX 11-AUG-1999; 99US-0148360P.

XX 13-DEC-1999; 99US-0170313P.

XX (CELL-) CELLONICS INC.

XX Rubin RA, Gough AH, Ghosh RN, Giuliano KA, Dunlay RT,

XX WPI; 2001-091619/10.

XX Identifying compounds modulating macromolecule trafficking through
 PT endosomes, using digital data obtained by converting a luminescent signal

PT from cells contacted with the compound.
 XX
 XX Example 6; Page 53; 113pp; English.

CC The present invention relates to an automated method for identifying
 CC compounds that induce or inhibit macromolecule trafficking through an
 CC endosomal system. The method comprises treating cells which possess a
 CC luminescently-tagged macromolecule, with a test compound, and obtaining
 CC luminescent signals from the cells. The signal is converted into digital
 CC data that is used to determine if the test compound has induced or
 CC inhibited the trafficking. The method can also be used to identify the
 CC extent of internalisation of membrane receptors, by fusing a labelled
 CC peptide epitope to the different domains of the receptor e.g. the
 CC extracellular domain and intracellular domain. The present invention is
 CC one such peptide epitope used in the method of the present invention

XX Sequence 6 AA:
 SQ

Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHHHHH 6
 1 HHHHHH 6

Db

RESULT 25
 AAE12713
 ID AAE12713 standard; peptide; 6 AA.

XX AAE12713;

XX 04-JAN-2002 (first entry)

XX HexHis tag used to construct human blyPH1-IL-2 fusion protein.

XX Tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer; breast;

XX ovary; lung; bladder; cytostatic; therapy; PH1 antibody.

XX Synthetic.

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US010589.

XX 30-MAR-2000; 2000US-00538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX N-PSDB; AAD20743.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1.
 XX Example 1; Page 36; 126pp; English.

CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region, or a
 CC complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film. MUC1-
 CC specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is a polypeptide (hexahis) tag
CC used for constructing human bIVPH1-IL-2 fusion protein which is an
CC immunocytokine MUC1-specific binding member
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 26

AAE13079 ID AAE13079 standard; peptide; 6 AA.

XX AAE13079;

DT 28-JAN-2002 (first entry)

DE Epitope tag #7 used in yeast cell surface display of proteins.

KW Phenotypic property; yeast; cell wall protein; epitope tag.

OS Unidentified.

PN US6300065-B1.

PD 09-OCT-2001.

PF 26-AUG-1998; 98US-00140084.

PR 31-MAY-1996; 96US-0018741P.

PR 30-MAY-1997; 97US-00866398.

PR 20-JAN-1998; 98US-00009388.

XX (UNII) UNIV ILLINOIS FOUNO.

PI Kieke MC, Wiltrop KD, Boder ET, Kranz DM, Shusta E;

DR WPI, 2001-656236/75.

XX Selecting proteins, e.g. antibodies, with enhanced phenotypic properties

PT relative to those of a wild-type comprises transforming yeast cells with

PT a vector expressing a protein to be tested fused to a yeast cell wall

PT protein.

PS Disclosure: Col 5; 64pp; English.

XX The present invention relates to a method for selecting proteins with

XX enhanced phenotypic properties relative to those of a wild-type,

CC comprises transforming yeast cells with a vector expressing a protein to

CC be tested fused to a yeast cell wall protein. The method is particularly

CC useful for selecting antibodies for improved affinity and specificity.

CC The present sequence is an epitope tag which is used in yeast cell

CC surface display of proteins

XX Sequence 6 AA;

Db 1 HHHHHH 6

RESULT 27

AAAB35439 ID AAB35439 standard; peptide; 6 AA.

XX AAB35439;

DT 23-MAY-2001 (first entry)

DE Nascent protein detection method related peptide #1.

KW Nascent protein detection; protein analysis; aminoacylated tRNA;

KW BODIPY marker; disease diagnosis.

OS Unidentified.

PN WO200114578-A1.

PD 01-MAR-2001.

PF 23-AUG-2000; 2000WO-US023233.

PR 25-AUG-1999; 99US-00382736.

PR 25-AUG-1999; 99US-00382950.

XX (AMBE-) AMBERGEN INC.

PI Rochschild KJ, Gite S, Olejnik J;

DR WPI, 2001-168972/17.

XX Method for detecting nascent proteins by fluorescence comprises

PT misaminoacylating a tRNA molecule with a marker compound, useful for

PT detecting mutations in proteins, e.g. cancer.

PS Example 22; Page 153; 204pp; English.

XX The present invention describes a method of detecting nascent proteins

CC involving aminoacylating a tRNA molecule with a 4,4-difluoro-4-bora-3a,4a

CC -diala-s-indacene (BODIPY) marker leading to the production of a

CC misaminoacylated tRNA. This enables the detection, isolation and analysis

CC of nascent proteins using UV without the usual accompanying radioactivity

CC problems. It may be used to detect mutations, for example in cancer,

CC Duchenne muscular dystrophy, adenomatous polyposis coli and colon cancer

XX Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 28

AAAB45989 ID AAB45989 standard; peptide; 6 AA.

XX AAB45989;

DT 02-APR-2001 (first entry)

DE Transdominant effector peptide associated screening peptide #68.

KW Intracellular transdominant bioactive agent; screening; cell phenotype;

XX effector peptide.

OS Unidentified.

PN US6153380-A.
 XX
 PD 28-NOV-2000.
 XX
 XX
 PF 23-JAN-1997; 97US-00789333.
 XX
 XX 23-JAN-1996; 96US-00589108.
 PR 23-JAN-1996; 96US-00589911.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX (RIGE-) RIGEL PHARM INC.
 XX
 P1 Rothenberg SM, Nolan GP;
 XX
 DR WPI; 2001-060084/07.
 XX
 XX
 PT Methode for screening intracellular transdominant effector peptides and
 PT RNA molecules comprise delivering random oligonucleotides to cells, which
 PT are then screened for an altered phenotype.
 XX
 PS Disclosure; Col 101-102; 57pp; English.
 XX
 CC This invention describes novel in vitro screening methods (1) for a
 CC transdominant intracellular bioactive agent capable of altering the
 CC phenotype of a cell. (1) comprises: (a) introducing a molecular library
 CC of randomized candidate nucleic acids into several cells; and (b)
 CC screening the cells for a cell exhibiting an altered phenotype, where the
 CC altered phenotype is due to the presence of a transdominant bioactive
 CC agent. The methods are particularly useful for screening intracellular
 CC transdominant effector peptides and RNA molecules selected inside living
 CC cells from randomized pools. (1) is also useful for introducing random
 CC libraries into cells to screen for bioactive compounds. The methods allow
 CC rapid and highly efficient screening of large numbers of random
 CC oligonucleotides and their corresponding expression products in a single
 CC step. In addition, the methods allow screening in the absence of
 CC significant prior characterization of the cellular defect
 XX
 SQ Sequence 6 AA;
 XX
 QY
 DB 1 HHHHHH 6
 1 HHHHHH 6
 1 HHHHHH 6
 RESULT 29
 AAG78043
 ID AAG78043 standard; peptide; 6 AA.
 XX
 AC AAG78043;
 XX
 DT 20-NOV-2001 (first entry)
 XX
 DE 6-His epitope tag.
 XX
 KW abnormal base-pairing; polymorphism; nucleic acid repair enzyme;
 KW mutation; infection; cancer; immune system disorder; metabolic disorder;
 KW muscle disorder; bone disorder; nervous system disorder;
 KW high throughput screening; epitope tag.
 XX
 OS Synthetic.
 XX
 PN WO200162968-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 05-JAN-2001; 2001WO-US000452.
 XX
 PR 25-FEB-2000; 2000US-00514016.
 XX

PA (GEAT) GEN ATOMICS.
 XX
 PI Yuan C;
 XX
 DR WPI; 2001-536643/59.
 XX
 XX
 PT Detecting abnormal base-pairing, mutation in nucleic acid, or
 PT polymorphism in gene locus, comprises contacting nucleic acid with
 PT abnormal base-pairing and mutant nucleic acid repair enzyme, and
 PT detecting their binding.
 XX
 PS Disclosure; Page 180; 294pp; English.
 XX
 CC The invention relates to detecting abnormal base-pairing in a nucleic
 CC acid duplex, mutation in a nucleic acid or polymorphism in a gene locus,
 CC comprising contacting a nucleic acid duplex having an abnormal base-
 CC pairing with a mutant nucleic acid repair enzyme or its complex and
 CC detecting the binding between the nucleic acid duplex and mutant enzyme,
 CC such that the presence of abnormal base-pairing, mutation or polymorphism
 CC is detected. The method is useful for prognosis or diagnosis of the
 CC presence or severity of a disease, disorder or infection by a
 CC pathological agent associated with the mutation, including cancer, immune
 CC system disorders, metabolic disorders, muscle and bone disorders, nervous
 CC system disorders, signal disorders and transporter disease or disorder.
 CC The method is rapid and accurate and is amenable to high throughput
 CC formats. The method requires neither specific probes nor gel
 CC electrophoresis and is amenable to automation for simultaneous detection
 CC of a large number of nucleic acid mutations. The present sequence is that
 CC of an epitope tag, useful to the invention
 XX
 SQ Sequence 6 AA;
 XX
 QY
 DB 1 HHHHHH 6
 1 HHHHHH 6
 1 HHHHHH 6
 RESULT 30
 AAB97353
 ID AAB97353 standard; peptide; 6 AA.
 XX
 AC AAB97353;
 XX
 DT 15-AUG-2001 (first entry)
 XX
 DE 6-His epitope used in dual labelled receptor construction.
 XX
 KW Automated measurement; cell viability; epitope tag; luminescence;
 KW G-protein coupled receptor; high content screen.
 XX
 OS Synthetic.
 XX
 PN WO200135072-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 09-NOV-2000; 2000WO-US030896.
 XX
 PR 09-NOV-1999; 99US-0164353P.
 PR 18-JAN-2000; 2000US-0176504P.
 XX
 PA (CELL-) CELLOMICS INC.
 XX
 PI Ghosh RN, Debiasio R, Chen Y, Bellutca P, Giuliano K, Pasley JW;
 XX
 DR WPI; 2001-329169/34.
 XX
 PT Automated measurement of cell viability, involves contacting cells with
 PT luminescent reporter molecule, imaging cells to get signals, converting

PT signals into digital data and using data to measure viable cell.
XX
PS Example 6; Page 52; 155pp; English.
XX
CC This invention relates to a method for the automated measurement of cell
CC viability. The method involves contacting cells with luminescent reporter
CC molecules, imaging cells to get signals, and converting the signals into
CC digital data which can be used as a measurement of cell viability.
CC Included in the invention is a computer readable storage medium
CC comprising a programme which causes the method of the invention to be
CC activated. The method is useful for cell state identification in cells.
CC The method is also useful for drug discovery. An example of the invention
CC relates to the use of inserted sequences and their ligands for high
CC content screens incorporating dual labelled receptors. The present
CC sequence represents an epitope tag used to label one end of a G-protein
CC coupled receptor (GPCR). The intracellular and extracellular domains of
CC the GPCR are distinctly labelled so that using the method of the
CC invention the extent of internalisation of the receptor can be measured
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;
QY 1 HHHHHH 6
DB 1 HHHHHH 6
RESULT 31
AAMS2173
ID AAMS2173 standard; peptide; 6 AA.
AC AAMS2173;
DT 07-FEB-2002 (first entry)
DE Peptide tag 1.
XX
XX Factor VII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW cardiant; hepatocytic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
OS Synthetic.
XX
XX WO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-DK000094.
XX
XX 11-FEB-2000; 2000DK-00000218.
XX
XX 18-OCT-2000; 2000DK-00001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX
XX WPI; 2001-581807/65.
XX
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as hemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently attached
XX to polypeptide group.
XX
XX Disclosure; Page 42; 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX polypeptide conjugates, comprising at least one non-polypeptide group
XX covalently attached to a polypeptide, where the amino acid sequence of
XX polypeptide differs from that of the wildtype FVIIa (AAMS2171) in that at
XX least one amino acid residue containing an attachment group for the non-

CC polypeptide group has been introduced or removed. The FVIIa conjugates
CC have haemostatic, thrombolytic, cardiant, hepatocytic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a peptide tag, useful
CC to the invention
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;
QY 1 HHHHHH 6
DB 1 HHHHHH 6
RESULT 32
ABB76820
ID ABB76820 standard; peptide; 6 AA.
AC ABB76820;
DT 16-JUL-2002 (first entry)
DE His tag.
XX
XX Angiopoietin-Y2; His tag.
XX
XX Unidentified.
XX
XX KR2000059883-A.
XX
XX 16-OCT-2000.
XX
XX 09-MAR-1999; 99KR-00007779.
XX
XX 09-MAR-1999; 99KR-00007779.
XX
XX (KOHG/) KOH G Y.
XX
XX (KIMI/) KIM I J.
XX
XX Kwak HJ, Ahn JE, Koh GN, Kim SY;
XX
XX WPI; 2001-254061/26.
XX
XX
XX Novel angiopoietin-Y2 gene and recombinant protein.
XX
XX Example 1; Page 4; 10pp; Korean.
XX
XX The present invention relates to a novel angiopoietin-Y2 gene and
XX recombinant protein. The present sequence is a His tag used in an example
XX from the invention
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;
QY 1 HHHHHH 6
DB 1 HHHHHH 6
RESULT 33
AAB66801

```

ID  AAB66801 standard; peptide; 6 AA.
XX
XX  AAB66801;
AC
XX  27-APR-2001 (first entry)
DT
XX  6-His epitope.
DE
XX  Analyte-binding enzyme; analyte analysis; epitope.
XX
XX  Undifferentiated.
OS
XX  WO200102600-A2.
PN
XX  11-JAN-2001.
PD
XX  30-JUN-2000; 2000WO-US018057.
PE
XX  06-JUL-1999; 99US-00347878.
PR  06-DEC-1999; 99US-00457205.
XX
XX  (GEAT ) GEN ATOMICS.
PA
XX  Yuan C;
PI
XX  WPI; 2001-071583/08.
DR
XX
XX  Assaying method, useful for prognosis and diagnosis of disease, comprises
PT  contacting sample with a mutant analyte-binding enzyme and detecting
PT  binding.
XX
XX  Disclosure; Page 104; 187pp; English.
XX
XX  The present invention relates to a method for assaying an analyte in a
CC  sample comprising: contacting the sample with a mutant analyte-binding
CC  enzyme which has binding affinity for the analyte or an immediate analyte
CC  enzymatic conversion product but has attenuated catalytic activity; and
CC  detecting resulting binding. The method is useful in monitoring
CC  biological systems/processes, or prognosis/diagnosis of disease caused by
CC  imbalances of the analytes. The present sequence is an epitope used in
CC  the present invention
XX
XX  Sequence 6 AA;
SQ
XX
XX  Query Match          100.0%; Score 48; DB 4; Length 6;
XX  Best Local Similarity 100.0%; Pred. No. 2e+06;
XX  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY
XX  1 HHHHHH 6
XX  |||||
XX  1 HHHHHH 6
Db
XX
XX  RESULT 34
XX  AAE01997
ID  AAE01997 standard; peptide; 6 AA.
XX
XX  AAE01997;
AC
XX  31-JUL-2001 (first entry)
DT
XX
XX  Poly-His tag used to prepare poly-His version of huRANKL.
XX
XX  Receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB;
XX  tumour necrosis factor; TNF; type I transmembrane protein;
XX  TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
XX  inflammatory reaction; bone resorption; gene therapy; immunomodulator;
XX  immune system dysfunction; familial expansile osteolysis; FEO;
XX  early onset Paget's disease of bone; BP; cytostatic; poly-his tag.
XX
XX  Synthetic.
OS
XX  WO200136637-A1.
PN

```

```

XX  25-MAY-2001.
PD
XX
XX  14-NOV-2000; 2000WO-US031459.
PF
XX
XX  17-NOV-1999; 99US-00442029.
PR
XX
XX  (IMNV ) IMMUNEX CORP.
PA
XX
XX  Anderson DM, Hughes AE;
PI
XX
XX  WPI; 2001-329222/34.
DR
XX
XX  New DNA encoding a receptor activator of NF-kappaB polypeptide for the
PT  treatment of Paget's disease and Familial Expansile Osteolysis (FEO).
PT
XX
XX  Example 15; Page 82; 96pp; English.
XX
XX  The present invention relates to a novel receptor, referred to as RANK
CC  (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
CC  (tumour necrosis factor) receptor superfamily. RANK is a Type I
CC  transmembrane protein that interacts with TNF receptor-associated factors
CC  (TRAFs). Triggering of RANK by overexpression or co-expression of RANK
CC  and membrane bound RANK ligand (RANKL) results in upregulation of the
CC  transcription factor NF-kappaB, a ubiquitous transcription factor that is
CC  most extensively utilized in cells of the immune system. Inhibition of NF
CC  -kappaB by RANK antagonists is useful in ameliorating negative effects of
CC  inflammatory reactions, and the effects of excess bone resorption. The
CC  RANK DNAs, proteins and their analogues are useful for the preparation of
CC  pharmaceutical compositions, for infecting target cells for use in gene
CC  therapy applications in diagnosing diseases associated with RANK, and as
CC  targets for use in screening assays. They may be used in the treatment or
CC  diagnosis of immune system dysfunction. The present invention also
CC  encompasses gene therapy methods to correct gene-activating mutations,
CC  associated with e.g. familial expansile osteolysis (FEO) and early onset
CC  Paget's disease of bone (BP). The present sequence is a synthetic poly-
CC  his tag used to prepare soluble, tagged, poly-his version of human RANKL
CC  protein
XX
XX  Sequence 6 AA;
SQ
XX
XX  Query Match          100.0%; Score 48; DB 4; Length 6;
XX  Best Local Similarity 100.0%; Pred. No. 2e+06;
XX  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY
XX  1 HHHHHH 6
XX  |||||
XX  1 HHHHHH 6
Db
XX
XX  RESULT 35
XX  AAG65669
ID  AAG65669 standard; peptide; 6 AA.
XX
XX  AAG65669;
AC
XX  07-JAN-2002 (first entry)
DT
XX
XX  His tag used for recombinant expression of FGF-like polypeptide.
XX
XX  Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic;
XX  fat deposition; vulnerability; antidiabetic; dermatological; anorectic;
XX  antidiabetic; antiinflammatory; cytostatic; hepatic; vitricide;
XX  neuroprotectant; pulmonary; gene therapy; vaccine; human.
XX
XX  Synthetic.
OS
XX  WO200172957-A2.
PN  04-OCT-2001.
XX
XX  02-APR-2001; 2001WO-IB000664.
PF
XX

```

PR 31-MAR-2000; 2000US-00540118.
 XX (ITOH/) ITOH N.
 XX
 XX Itoh N;
 PI
 DR WPI; 2001-611623/70.
 XX
 PT New human nucleic acid encoding fibroblast growth factor-like peptide,
 PT useful for treatment and diagnosis of e.g. wounds and inflammatory bowel
 PT disease.
 XX
 XX Example 3; Page 117; 172pp; English.
 XX
 CC The invention provides human nucleic acids encoding fibroblast growth
 CC factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by
 CC standard recombinant methodology and are mitogenic for a wide range of
 CC cells, inducing differentiation and proliferation, and inhibiting
 CC deposition of fat. The FGF-like polypeptides, polynucleotides and
 CC specific antibodies and modulators are useful for treating a very wide
 CC range of diseases and conditions, e.g. wounds, ulcers, skin aging, viral
 CC obesity, diabetes, alopecia, inflammatory bowel disease, emphysema, viral
 CC hepatitis, multiple sclerosis, respiratory distress syndrome, tumors of
 CC the eye, etc., also for maintaining organs before transplant and
 CC supporting culture of primary cells and tissues. Sequences AAG6568-69
 CC represent amino acid sequences of protein tags used for recombinant
 CC expression of FGF-like polypeptide
 XX
 SO Sequence 6 AA;
 Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 1 HHHHHH 6

RESULT 36
 AAU00163
 ID AAU00163 standard; peptide; 6 AA.
 XX
 AC AAU00163;
 XX
 DT 16-MAY-2001 (first entry)
 XX
 DE His Tag for purification of interferon beta fusion proteins.
 XX
 KW Human; interferon beta; antibody; multiple sclerosis; gene therapy;
 KW viral infection; viral hepatitis; cancer; breast cancer; inflammation;
 KW Crohn's disease; acute myeloid leukaemia; Hodgkin's disease;
 KW ulcerative colitis; immunomodulation; His tag.
 XX
 OS Synthetic.
 XX
 PN WO200115736-A2.
 PD 08-MAR-2001.
 PF 25-AUG-2000; 2000WO-DK000471.
 XX
 PR 27-AUG-1999; 99DK-00001197.
 PR 21-OCT-1999; 99US-0160782P.
 PR 26-NOV-1999; 99DK-00001691.
 PR 07-FEB-2000; 2000DK-00000194.
 PR 07-MAR-2000; 2000DK-00000363.
 PR 14-APR-2000; 2000DK-00000642.
 XX
 PA (MAXY-) MAXYGEN APS.
 XX
 PI Pedersen AH, Schambye HT, Andersen KV, Bornaes C, Rasmussen PB;
 XX

DR WPI; 2001-218488/22.
 XX
 XX A conjugate exhibiting interferon beta activity useful for treating
 PT multiple sclerosis comprises a non-polypeptide group covalently attached
 PT to an interferon beta polypeptide.
 XX
 XX Disclosure; Page 40; 108pp; English.
 PS
 CC The sequence is a His tag suitable for purification of Human interferon
 CC beta fusion proteins and to facilitate conjugation to a non-polypeptide
 CC moiety. Conjugates of the invention exhibiting interferon beta activity
 CC comprise at least one first non-polypeptide group covalently attached to
 CC an interferon beta polypeptide, the amino acid sequence of which differs
 CC from wild-type human interferon beta in at least one introduced and at
 CC least one removed amino acid residue comprising an attachment group for
 CC the first non-polypeptide group. The invention also concerns reducing the
 CC immunogenicity and/or increasing functional in vivo half-life and/or
 CC serum half-life of an interferon beta polypeptide comprising introducing
 CC an amino acid residue constituting an attachment group for a first non-
 CC polypeptide group into a position exposed at the surface of the protein
 CC that does not contain such a group and removing an amino acid residue
 CC constituting an attachment group for a first non-polypeptide group and
 CC subjecting the modified peptide to conjugation with the non-polypeptide
 CC group. The conjugate and a cell culture expressing the mutated
 CC polypeptides are useful in the treatment of disease, especially multiple
 CC sclerosis, and for treating mammals having circulating antibodies against
 CC interferon beta 1a or 1b. DNA encoding the mutated proteins may be used
 CC for gene therapy. The DNA and proteins can also be used to treat viral
 CC infections (e.g. viral hepatitis), cancer (e.g. breast cancer),
 CC inflammation, Crohn's disease, acute myeloid leukaemia, Hodgkin's disease
 CC and ulcerative colitis and for immunomodulation
 XX
 SO Sequence 6 AA;
 Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 1 HHHHHH 6

RESULT 37
 AAG62605
 ID AAG62605 standard; peptide; 6 AA.
 XX
 AC AAG62605;
 XX
 DT 06-SEP-2001 (first entry)
 XX
 DE Metal capturing protein related peptide #2.
 XX
 KW Metal capturing protein; metal capture; secretory signal;
 KW waste treatment.
 XX
 OS Synthetic.
 XX
 PN WO200138517-A1.
 PD 31-MAY-2001.
 PF 26-OCT-2000; 2000WO-JP007518.
 XX
 PR 19-NOV-1999; 99JP-00330226.
 XX
 PA (TOYOTA) TOYOTA JIDOSHA KK.
 XX
 PI Tanaka A, Ueda M;
 XX
 DR WPI; 2001-355927/37.
 DR N-PSDB; AAH45709.
 XX

PT Fused gene with DNA expressing polypeptide capable of capturing metal,
PT for recombinant vectors and transformants applicable in purifying
PT environment and recovering metal efficiently, including waste treatment.
XX
PS Claim 4; Page 32; 45pp; Japanese.
XX
CC The present invention relates to a fused gene containing DNA encoding a
CC secretory signal peptide, a protein capable of capturing a metal and a
CC protein localised on the cell surface. The gene can be used to express
CC the metal capturing protein, which can then be used in purifying and
CC recovering metal, for example in waste treatment. The present sequence is
CC a peptide described in the exemplification of the invention
XX
SQ Sequence 6 AA;
XX
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
Db 1 HHHHHH 6
XX
RESULT 38
AAB62662
ID AAB62662 standard; peptide; 6 AA.
XX
AC AAB62662;
XX
DT 23-JUN-2001 (first entry)
XX
DE C-terminal HIS tag.
XX
KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW antirheumatic; antirheumatic; antiaesthetic; antiatherosclerotic;
KW immunosuppressive; chromosome 6q24.1-25.2; human.
XX
OS Synthetic.
XX
PN WO200140467-A1.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032703.
XX
PR 03-DEC-1999; 99US-0169049P.
PR 13-SEP-2000; 2000US-0232219P.
PR 31-OCT-2000; 2000US-0244610P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
DR WPI; 2001-356158/37.
XX
PT New soluble cytokine receptor polypeptides and polynucleotides, useful
PT for diagnosing and treating cancer and inflammatory conditions.
XX
PS Example 1; Page 193; 210pp; English.
XX
CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cells (progenitors); reducing IL-
CC TIF induced or IL-9 induced inflammation; and suppressing an inflammatory
CC response in a mammal with inflammation. Heteromeric/ multimeric receptor
CC polypeptides such as soluble zcytor 16/CRP2-4 can be used to reduce
CC progression and symptoms of cancer. Zcytor16 polypeptides can also be
CC used to detect IL-TIF levels which is indicative of pathological
CC conditions including inflammatory states (e.g. Rheumatoid arthritis) and
CC cancer. Antibodies that bind zcytor16 polypeptides and the polypeptides

CC themselves are useful for the treatment of inflammation, inflammatory
CC diseases (e.g. infection, asthma, inflammatory bowel disease, rheumatoid
CC arthritis and atherosclerosis) and autoimmune diseases. The antibodies
CC and zcytor16 polynucleotides are also useful for detecting cancer. The
CC present sequence represents a C-terminal HIS tag, used in the
CC construction of a zcytor16 mammalian expression vector
XX
SQ Sequence 6 AA;
XX
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
Db 1 HHHHHH 6
XX
RESULT 39
AAU02090
ID AAU02090 standard; peptide; 6 AA.
XX
AC AAU02090;
XX
DT 07-SEP-2001 (first entry)
XX
DE His-tag peptide.
XX
KW Fibroblast growth factor 20; FGF-20; Parkinson's disease;
KW subcutanea nigra; dopaminergic neuron; cochlea-associated disease;
KW otosclerosis; Cogan's syndrome; Meniere's disease; Pendred's syndrome;
KW diabetes-associated hearing loss; congenital malformations;
KW autoimmune disease-related hearing loss; age-related hearing loss;
KW deafness; ischaemia-related hearing disturbance; immunogen; antibody;
KW neuro-degenerative disease; tendonitis; wound healing; stroke; ischaemia;
XX
OS Synthetic.
XX
PN WO200131008-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US029237.
XX
PR 22-OCT-1999; 99US-0161162P.
PR 08-MAR-2000; 2000US-0187856P.
XX
PA (CHIR) CHIRON CORP.
XX
PI (KYOU) UNITIV KYOTO.
XX
PI Itoh N, Kavanaugh WM;
XX
DR WPI; 2001-308642/32.
XX
PT New human and rat fibroblast Growth Factor (FGF) polypeptides for
PT providing trophic support for cells used in Parkinson patients, and
PT alleviating brain and cochlea conditions.
XX
PS Example 6; Page 44; 73pp; English.
XX
CC The sequence an His-tag which can be incorporated into a fusion protein
CC (to allow purification of the fusion protein) with Human or rat
CC fibroblast growth factor 20, FGF-20. The FGF polypeptides and nucleic
CC acids encoding them are useful for providing trophic support for cells in
CC a patient, especially a patient with Parkinson's disease, and FGF-20 is
CC additionally used to treat patients with conditions of the substantia
CC nigra. The polypeptides and nucleic acids are useful for alleviating
CC human brain conditions by slowing degeneration, restoring function of,
CC increasing the number of, dopaminergic neurons. The polypeptides and
CC nucleic acids are also useful for alleviating cochlea-associated disease
CC by slowing degeneration of or restoring or maintaining normal function of
CC the structure of cochlea, where the disease is otosclerosis, Cogan's

CC syndrome, Meniere's disease, Pendred's syndrome, diabetes-associated
CC hearing loss, congenital malformations, autoimmune disease-related
CC hearing loss, age-related hearing loss, deafness associated with lack of
CC FGF receptor and ischaemia-related hearing disturbance. Other diseases
CC thought to be amenable to FGF therapeutic activity include neuro-
CC degenerative diseases, tendonitis, wound healing, stroke and ischaemia.
CC The polypeptides can be used to screen for agonists and antagonists.
CC Epitope bearing fragments of the FGF-20 polypeptides can be used to raise
CC anti-FGF-20 antibodies
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 1 HHHHHH 6
RESULT 40
AAB85699 standard; peptide; 6 AA.
ID AAB85699 standard; peptide; 6 AA.
XX AAB85699;
AC AAB85699;
XX 29-OCT-2001 (first entry)
DT 29-OCT-2001 (first entry)
XX Amino acid sequence of six-histidine epitope tag.
DE Multivalent protein; immune response; Plasmodium vivax; parasite;
XX protozoacide; vaccine; malaria; recombinant; ViVac1; ViVac2.
KW Synthetic.
OS WO200155181-A2.
XX 02-AUG-2001.
XX 29-JAN-2001; 2001WO-US002937.
XX 31-JAN-2000; 2000US-0179213P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA La1 AA, Xiao L, Zhou Z;
XX WPI; 2001-514557/56.
DR WPI; 2001-514557/56.
XX New recombinant multivalent protein comprising antigenic determinants
PT derived from more than one stage in a life cycle of Plasmodium vivax,
PT useful as a vaccine for treating, preventing and reducing malarial
PT infection.
XX Example 1; Page 25; 59pp; English.
PS The invention relates to recombinant multivalent proteins (I) that
XX stimulate an immune response to Plasmodium vivax. (I) comprises antigenic
CC determinants, fragments or conservative substitutions, derived from more
CC than one stage in a life cycle of a Plasmodium vivax parasite. (I) is
CC useful as a vaccine for stimulating an immune response, specifically a
CC protective immune response that confers increased resistance to infection
CC by Plasmodium parasites, such as P. vivax. (I) is especially useful in
CC the treatment, prevention and reduction of malarial infection, as
CC research or diagnostic reagents for the detection of Plasmodium species
CC in a biological sample, and for conferring immunity against multiple
CC stages of the malarial parasite. The antibodies produced are useful for
CC the detection or measurement of antigenic epitopes derived from one or
CC more stages in a life cycle of a parasite, particularly P. vivax. The
CC vaccine comprising the recombinant proteins, is cost-effective, health-
CC promoting intervention for controlling, preventing or treating the
CC incidence of malaria. The present sequence represents the amino acid

CC sequence of a six-histidine epitope tag, a component of the multivalent
CC and multistage proteins ViVacip and ViVac2p
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 1 HHHHHH 6
RESULT 41
ABR00924 standard; peptide; 6 AA.
ID ABR00924 standard; peptide; 6 AA.
XX ABR00924;
AC ABR00924;
XX 03-APR-2003 (first entry)
DT 03-APR-2003 (first entry)
XX Hexahistidine peptide tag SEQ ID NO 32.
DE Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;
KW antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;
KW obesity; inflammatory bowel disease.
OS Synthetic.
XX WO200178894-A2.
XX 25-OCT-2001.
XX 13-APR-2001; 2001WO-US012245.
XX 13-APR-2000; 2000US-00548797.
XX (GENO-) GENOME THERAPEUTICS CORP.
PA Keith T;
XX WPI; 2001-639428/73.
DR WPI; 2001-639428/73.
XX Isolated genes (Gene 216) from human chromosome 20p13-p12 and the
PT proteins they encode, useful for the prevention, diagnosis and treatment
PT of asthma, obesity and inflammatory bowel disease.
PS Disclosure; Page 45; 520pp; English.
XX The invention relates to isolated genes (Gene 216) from human chromosome
CC 20p13-p12 and the proteins they encode. The nucleic acids and proteins
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate Gene 216 expression. For example, the
CC nucleic acids (or vectors) and proteins may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of gene 216 by expressing
CC inactive proteins or to supplement the patient's own production of Gene
CC 216 proteins. Additionally, the nucleic acids may be used to produce the
CC secreted Gene 216 protein, by inserting the nucleic acids into a host
CC cell and culturing the cell to express the protein. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acid
CC sequences in samples and therefore which patients may be in need of
CC restorative therapy. The Gene 216 protein may also be used as antigens in
CC the production of antibodies against Gene 216 and in assays to identify
CC modulators of Gene 216 expression and activity. The anti-Gene 216
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. The anti-Gene 216 antibodies may also be used as diagnostic
CC agents for detecting the presence of Gene 216 proteins in samples (e.g.
CC by enzyme linked immunosorbent assay or ELISA). Disorders that may be
CC prevented, diagnosed and/or treated by the above methods include, for
CC example asthma, obesity and inflammatory bowel disease. The present

CC sequence is that of a peptide tag used in analysis of the Gene 216
 CC encoded protein
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 1 HHHHHH 6
 DB

RESULT 42
 AAE08006
 ID AAE08006 standard; peptide; 6 AA.

AC AAE08006;

DT 01-NOV-2001 (first entry)

XX His tag useful as antibody recognition sequences.

DE Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
 XX transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
 KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
 KW locomotor; anxiety disorder; limbic seizure; tranquilliser; his tag.

XX Unidentified.

OS WO200155103-A2.

XX 02-AUG-2001.

XX 29-JAN-2001; 2001WO-US002804.

XX 28-JAN-2000; 2000US-0178652P.

XX (NEUR-) NEUROGEN CORP.

XX Bennett M, Brodbeck R, Krause J;

XX WPI; 2001-514543/56.

PT New chimeric receptor proteins comprising a single polypeptide chain of
 PT amino acids, useful as targets for drug actions, and as basis for drug
 PT discovery and development.

XX Disclosure; Page 54; 72pp; English.

XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.
 CC The NPY receptors are G-protein-coupled transmembrane proteins with seven
 CC membrane spanning transmembrane (TM) domains. The compounds that modulate
 CC the activity of a NPY receptor is useful in the preparation of a
 CC medicament for treating conditions including obesity, high/low blood
 CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
 CC seizure, locomotor and anxiety disorders. They can also be used as
 CC targets for drug actions, and as basis for drug discovery and
 CC development. The NPYs receptor may have an anti-epileptic activity in the
 CC control of limbic seizures. The present sequence is a hexa-histidine (His
 CC -6x) tag which is used as antibody recognition sequences in the
 CC exemplification of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 1 HHHHHH 6
 DB 1 HHHHHH 6

RESULT 43
 AAM51720
 ID AAM51720 standard; peptide; 6 AA.

AC AAM51720;

DT 29-JAN-2002 (first entry)

DE FSH alpha or beta tagging peptide 1.

XX Human, FSH alpha; FSH beta; follicle stimulating hormone; glycosylation;
 KW antifertility.

OS Synthetic.

XX WO200158493-A1.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-DK000090.

XX 11-FEB-2000; 2000DK-00000220.

XX 14-JUL-2000; 2000DK-00001092.

XX (MAXY-) MAXYGEN APS.

PI Schambye HT, Andersen KV, Van Den Hazel B, Christiansen J;

PI Jeppesen CB;

XX WPI; 2001-607186/69.

PT New polypeptide conjugate with follicle stimulating hormone (FSH)
 PT activity, used to treat infertility, comprises polypeptide having
 PT modified FSH alpha and beta subunits with attachment group for non-
 PT polypeptide moiety.

XX Disclosure; Page 37; 88pp; English.

XX The invention relates to new polypeptides and polypeptide conjugates
 CC exhibiting follicle stimulating hormone (FSH) activity. FSH is a dimeric
 CC hormone comprising of an alpha (AAM51709) and beta (AAM51711) subunit.
 CC The invention relates to a heterodimeric FSH conjugate comprising, a
 CC dimeric polypeptide having FSH alpha (AAM51733-AAM51800, AAM51442-
 CC AAM51449) and beta (AAM52001-AAM52104) subunits, where at least one
 CC subunit differs from corresponding wild-type subunit in that an amino
 CC acid residue containing an attachment group for a non-polypeptide
 CC molecule has been introduced or removed, especially where at least one of
 CC the FSH-alpha and FSH-beta subunits comprises at least one introduced N-
 CC or O-glycosylation site at its N-terminal and the glycosylation site
 CC being glycosylated. The polypeptides have antifertility activity. The
 CC polypeptides have increased functional in vivo half life and/or serum
 CC half life as compared to human FSH, replenishing insufficient endogenous
 CC FSH production in a patient. The present sequence is that of a peptide
 CC tag for protein purification

XX Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 1 HHHHHH 6
 DB 1 HHHHHH 6

RESULT 44
 AAE26107
 ID AAE26107 standard; peptide; 6 AA.

AC AAE26107;

XX 14-NOV-2002 (first entry)
 XX His tag peptide used to generate soluble human RANKL protein.
 DE
 XX
 XX RANK; receptor activator of nuclear factor-kappaB; NF-kB; sepsis;
 KW immune response; toxic shock; graft-versus-host reaction; therapy; TRAF;
 KW tumour necrosis factor receptor-associated factor; immunosuppressive;
 KW antibacterial; antiinflammatory.
 XX
 OS Synthetic.
 XX
 PN US2002086827-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 30-MAY-2001; 2001US-00871291.
 XX
 PR 23-DEC-1996; 96US-0059978P.
 PR 07-MAR-1997; 97US-0077181P.
 PR 14-OCT-1997; 97US-0064671P.
 PR 22-DEC-1997; 97US-0099613P.
 PR 17-DEC-1999; 99US-00466496.
 PR 24-MAY-2000; 2000US-00577800.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM;
 XX
 DR WPI; 2002-642254/69.
 XX
 XX A novel RANK (receptor activator of nuclear factor-kappaB (NF-kB))
 PT polypeptide, useful for inhibiting activation of NF-kB and for regulating
 PT an immune or inflammatory response in an individual.
 XX
 PS Example 15; Page 40; 49pp; English.
 XX
 CC The invention relates to novel RANK (receptor activator of nuclear factor
 CC -kappaB (NF-kB)) proteins and polynucleotides encoding them. Sequences of
 CC the invention are useful for inhibiting activation of NF-kappaB. They are
 CC useful for regulating an immune or inflammatory response in an individual
 CC at risk for an immune or inflammatory response. Inhibition of NF-kappaB
 CC by RANK antagonists is useful in ameliorating negative effects of an
 CC inflammatory response that results from triggering of RANK, for e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions or acute
 CC inflammatory reactions. Soluble RANK is useful as an adjunct therapy for
 CC diseases characterised by neoplastic cells that express RANK. Soluble
 CC forms of the receptor are useful in vitro to screen for agonists or
 CC antagonists of RANK activity. The cytoplasmic domain of RANK is useful in
 CC developing assays for inhibitors of signal transduction, to screen for
 CC molecules that inhibit interaction of RANK with tumour necrosis factor
 CC receptor-associated factor (TRAF) 2 or TRAF3. The present sequence is a
 CC His tag peptide used to generate a soluble, tagged, poly-His version of
 CC human RANK ligand (RANKL) protein. This peptide is used in the
 CC exemplification of the invention
 XX
 SQ Sequence 6 AA;
 XX
 QY Query Match 100.0%; Score 48; DB 5; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 DB Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 HHHHHH 6
 XX 1 HHHHHH 6
 XX
 RESULT 45
 ID AAE28476 standard; peptide; 6 AA.
 XX
 AC AAE28476;
 XX

DT 27-DEC-2002 (first entry)
 XX
 DE 6HTS peptide used for transfection enhancement.
 XX
 XX Tat region; nucleic acid-binding group; cell transfection system; cancer;
 KW gene therapy.
 XX
 OS Unidentified.
 XX
 PN US6376248-B1.
 XX
 PD 23-APR-2002.
 XX
 PF 16-MAR-1998; 98US-00039780.
 XX
 PR 14-MAR-1997; 97US-00818200.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hawley-Nelson P, Lan J, Shih P, Jesse JA, Schifferli KP,
 PI Gebeyehu G, Ciccarone VC, Evans KL;
 DR WPI; 2002-680647/73.
 XX
 PT New peptide comprising Tat sequence linked to nucleic acid-binding group,
 PT useful, e.g. in gene therapy, for improving cell-transfection efficiency.
 XX
 PS Example 1; Col 171-172; 108pp; English.
 XX
 CC The invention relates to a peptide comprising Tat sequence linked to
 CC nucleic acid-binding group. Peptides of the invention are used as
 CC components of a cell transfection system particularly for gene therapy
 CC (especially of cancer). The present sequence is a chimeric peptide useful
 CC for transfection enhancement. This peptide contains a His tail and a RGD
 CC peptide. This sequence is used in the exemplification of the invention
 XX
 SQ Sequence 6 AA;
 XX
 QY Query Match 100.0%; Score 48; DB 5; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 DB Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 HHHHHH 6
 XX 1 HHHHHH 6
 XX
 RESULT 46
 ID AAM49702 standard; peptide; 6 AA.
 XX
 AC AAM49702;
 XX
 DT 28-MAY-2002 (first entry)
 XX
 DE KpnI/SalI His-tag region.
 XX
 KW US6 gene; immunodominant; glycoprotein D; antigen; serological testing.
 XX
 OS Unidentified.
 XX
 PN RU2178806-C2.
 XX
 PD 27-JAN-2002.
 XX
 PF 21-JAN-2000; 2000RU-00101648.
 XX
 PR 21-JAN-2000; 2000RU-00101648.
 XX
 PA (VECT-) VECTOR VIROLOGY & BIOTECHN RES CENTRE.
 XX
 PI Susloparov MA, Susloparov IM, Plyasunov IV;
 XX

DR WPI; 2002-194324/25.
DR N-PSDB; ABA93644.
XX
PT Recombinant plasmid DNA phavd1 determining expression of gene US6
PT fragment of herpes simplex type-1 virus encoding immunodominant group of
PT glycoprotein d(gd)hsv-1 in bacterium Escherichia coli cells.
XX
PS Disclosure; Col 7; 9pp; Russian.
XX This invention describes a novel recombinant plasmid DNA constructed in
CC vitro and containing the herpes simplex type-1 virus (HSV-1) US6 gene
CC fragment which encodes an immunodominant group of glycoprotein D (gd).
CC This polypeptide shows the antigenic properties of herpes simplex virus
CC type-1. Purified recombinant protein can be used as HSV-1 antigen for the
CC serological testing of HSV-1 in clinical practice. This sequence
CC represents a His-tag sequence useful to the invention
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHHHHH 6
Db 1 HHHHHH 6
RESULT 47
AAU10567
ID AAU10567 standard; peptide; 6 AA.
XX
AC AAU10567;
XX
DT 14-FEB-2002 (first entry)
XX
DE Purification peptide tag.
XX
KW Compound library screening; signal transduction; peptide tether;
KW cellular receptor; reporter molecule.
XX
OS Synthetic.
XX
PN US6109842-B1.
XX
PD 30-OCT-2001.
XX
PF 24-NOV-1997; 97US-00977378.
XX
PR 03-DEC-1996; 96US-00758307.
XX
PA (GLAX) GLAXO WELLCOME INC.
XX
PI Dower WJ, Gates CM, Heinkei GL, Lalonde G, Matcheakis LC;
PI Paddon CJ, Schatz PJ;
XX
DR WPI; 2002-048370/06.
XX
PT Screening compounds having capacity to transduce signal through cellular
PT receptor by contacting complexes having test compound and tether
PT susceptible to modification with cell having receptor and reporter
PT molecule.
XX
PS Disclosure; Fig 6; 50pp; English.
XX
XX The invention relates to screening compounds for the capacity to
CC transduce a signal through a cellular receptor, by contacting complexes
CC having a test compound, a tag recording a step in synthesis of the
CC screened compound and a tether susceptible to modification by a reporter
CC molecule with cells having a receptor and a DNA fragment encoding the
CC reporter. Modification of the tether indicates that the complex contains
CC the compound. Supports must be provided, each bearing multiple copies of
CC a test compound and a tether, and are contacted with cells in order to

CC free a portion of the multiple copies of each of the compounds under test
CC from the supports. At least one compound transduces a signal through the
CC receptor of a cell causing expression of the reporter molecule, and
CC isolating the support having the modified tether, which support bears the
CC compound transducing the signal. An array of compounds can also be
CC provided on a membrane, which is contacted with a cell, where at least
CC one compound transduces a signal through the cell receptor, causing
CC expression of the reporter molecule, which is released from the cell, and
CC modifies the membrane at a position proximate to the compound transducing
CC the signal. The modification of the membrane allows identification and
CC isolation of the compound transducing the signal. The methods are useful
CC for the identification of compounds with desired properties, allowing the
CC isolation of novel pharmaceuticals. This sequence represents a
CC purification peptide tag of the invention
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHHHHH 6
Db 1 HHHHHH 6
RESULT 48
ABG32021
ID ABG32021 standard; peptide; 6 AA.
XX
AC ABG32021;
XX
DT 15-NOV-2002 (first entry)
XX
DE Synthetic protein tag, #1.
XX
XX Tag; single-chain multimeric polypeptide; polyethylene glycol; PEG;
KW granulocyte colony stimulating factor; G-CSF; hematopoietic disorder;
KW radiation therapy; chemotherapy; bone marrow transplantation;
KW acquired immunodeficiency syndrome; AIDS; immunodeficiency disease;
KW leukopenia; acute myeloid leukemia; half-life; clearance;
KW immunogenicity; bioavailability; single chain G-CSF dimer; HIV;
KW antihuman immunodeficiency virus; haemostatic.
XX
OS Synthetic.
XX
PN WO200236626-A1.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-DK000724.
XX
PR 02-NOV-2000; 2000DK-00001647.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Nissen TL, Jensen AD;
XX
DR WPI; 2002-618972/66.
XX
PT Single chain multimeric polypeptide conjugate for treating hematopoietic
PT disorders, has two units of monomeric polypeptides linked via peptide
PT bond/linker and polymer group bound to attachment group of polypeptide.
XX
PS Disclosure; Page 43; 108pp; English.
XX
XX The invention discloses a single-chain multimeric polypeptide conjugate
CC comprising at least two units of a monomeric polypeptide linked via a
CC peptide bond or a peptide linker, where the monomeric polypeptide is
CC biologically active in its monomeric form and has at least one polymer
CC group covalently bound to an attachment group of the polypeptide e.g.
CC polyethylene glycol (PEG). The polypeptide is preferably a single-chain

CC multimeric granulocyte colony stimulating factor (G-CSF) polypeptide
 CC comprising at least two G-CSF polypeptide monomers, linked via a peptide
 CC bond or a peptide linker, where at least one of the monomers is a variant
 CC of wild-type human G-CSF comprising at least one amino acid residue
 CC modification. The monomeric and multimeric polypeptides are useful in
 CC therapy and for manufacture of a medicament for treatment of general
 CC haematopoietic disorders, including disorders arising from radiation
 CC therapy, chemotherapy or bone marrow transplantations, acquired
 CC immunodeficiency syndrome (AIDS) or other immunodeficiency diseases,
 CC leukopenia and acute myeloid leukemia. The conjugate has one or more
 CC important properties as compared to the native polypeptide, including
 CC increased functional in vivo half-life, increased serum half-life,
 CC reduced clearance, reduced immunogenicity and/or increased
 CC bioavailability. Consequently, medical treatment with a conjugate offers
 CC advantages including longer duration between injections and fewer side
 CC effects. The sequence presented is the synthetic protein tag, #1, which
 CC can be used for purification of the single chain G-CSF dimer or aid
 CC conjugation with a non-polypeptide moiety

CC Sequence 6 AA;

Query Match 100.0%; Score 48; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||

Db 1 HHHHHH 6

RESULT 49
 AAE23795
 ID AAE23795 standard; peptide; 6 AA.

AC AAE23795;

DT 10-SEP-2002 (first entry)

DE His6 tag used in the invention.

XX Human; interleukin-17 related protein; inflammation mediated disorder;
 KW LP-48; asthma; allergic conjunctivitis; allergic rhinitis; cirrhosis;
 KW allograft rejection; Alzheimer's disease; chronic bronchitis; ARDS;
 KW gastritis; adult respiratory distress syndrome; contact dermatitis;
 KW Crohn's disease; glomerulonephritis; graft versus host disease; GVHD;
 KW hepatitis; hypertension; irritable bowel syndrome; myasthenia gravis;
 KW migraine; osteoarthritis; pancreatitis; rheumatoid arthritis; sepsis;
 KW septic shock; Sjogren's syndrome; systemic lupus erythematosus; burn;
 KW SLE; acne; ulcerative colitis; uveitis; autoimmune disorder; psoriasis;
 KW insulin-dependent diabetes mellitus; cancer; multiple sclerosis; AIDS;
 KW transplant rejection; anaemia; medical disorder; atherosclerosis; HIV;
 KW T-cell mediated condition; human immunodeficiency virus; lymphoma.

XX Synthetic.

OS WO20023083-A2.

PN 25-APR-2002.

PF 28-SEP-2001; 2001WO-US027737.

PR 13-OCT-2000; 2000US-0240177P.

PR 03-AUG-2001; 2001US-0309336P.

XX (EHLI) LILLY & CO EHI.

PI Glasebrook AL, Liu L, Newton CM, Tetreault JW;

DR WPI, 2002-444244/47.

XX Treating or preventing an inflammation mediated disorder or autoimmune
 PT disorder, or a T cell or Th2 cell mediated condition in a mammal,
 PT comprises administering interleukin-17 related polypeptide, LP-48 or its

PT antagonist.
 XX Disclosure, Page 17; 112pp; English.

CC The present invention relates to a method for treating or preventing
 CC inflammation mediated or autoimmune disorder, disorder associated with
 CC endothelial cell apoptosis and T or Th2 cell mediated condition. The
 CC method involves administering human interleukin-17 related polypeptide,
 CC LP-48 or its analogue/homologue or antagonist to a mammal. The method is
 CC useful for treating or preventing inflammation mediated disorders such as
 CC acne, allergic conjunctivitis, allergic rhinitis, allograft rejection,
 CC Alzheimer's disease, adult respiratory distress syndrome (ARDS), asthma,
 CC burns, chronic bronchitis, cirrhosis, contact dermatitis, Crohn's
 CC disease, gastritis, glomerulonephritis, graft-versus-host disease
 CC (GVHD), hepatitis, hypertension, irritable bowel syndrome, migraine,
 CC myasthenia gravis, osteoarthritis, pancreatitis, rheumatoid arthritis,
 CC sepsis, septic shock, Sjogren's syndrome, systemic lupus erythematosus
 CC (SLE), ulcerative colitis, uveitis and chronic inflammation), autoimmune
 CC disorders such as psoriasis, insulin-dependent diabetes mellitus, cancer,
 CC multiple sclerosis, transplant rejection, fulminant viral hepatitis B,
 CC and aplastic anaemia), medical disorders associated with endothelial cell
 CC apoptosis (e.g. atherosclerosis), and T-cell mediated condition (such as
 CC human immunodeficiency virus (HIV)-induced lymphoma or AIDS). The
 CC present sequence is his6 tag used in the invention

CC Sequence 6 AA;

Query Match 100.0%; Score 48; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||

Db 1 HHHHHH 6

RESULT 50
 AAE28606
 ID AAE28606 standard; peptide; 6 AA.

AC AAE28606;

DT 27-DEC-2002 (first entry)

DE His peptide tag.

XX Cytokine receptor; Zcytor16; IL-11F; autoimmune disease; dermatological;
 KW inflammatory disease; inflammatory bowel disease; rheumatoid arthritis;
 KW asthma; systemic lupus erythematosus; myasthenia gravis; pancreatitis;
 KW diabetes; atherosclerosis; glomerulonephritis; gene therapy; cystostatic;
 KW immunosuppressive; nephrotropic; allergy; placental health; abortion;
 KW cancer.

XX Synthetic.

OS WO200270655-A2.

PN 12-SEP-2002.

PF 04-MAR-2002; 2002WO-US006267.

PR 02-MAR-2001; 2001US-0273035P.

PR 27-MAR-2001; 2001US-0279232P.

XX (ZYMO) ZYMOGENETICS INC.

PI Presnell SR, Xu W, Kindsvogel W, Chen Z;

DR WPI, 2002-698750/75.

XX New Zcytor16 polypeptide useful for treating autoimmune or inflammatory
 PT diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma,
 PT atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects

PT of IL-TIF.

XX
PS
XX Example 1; Page 195; 221pp; English.

CC The invention relates to cytokine receptor designated as mouse Zcytor16
CC which can bind and antagonise the IL-TIF. The Zcytor16 polypeptide is
CC useful in modulating the immune system by binding Zcytor16 ligand, and
CC thus, preventing the binding of the ligand with endogenous Zcytor16
CC receptor. It is useful for studying human inflammatory or immune
CC function, or for treating autoimmune or inflammatory diseases such as
CC inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus
CC erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer,
CC diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic
CC aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-
CC Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the
CC anti-mouse Zcytor16 antibody are useful as probes in detecting gene
CC expression and gene structure, such as in the diagnosis and/or prevention
CC of spontaneous abortions or in monitoring placental health and function.
CC It is also used in gene therapy. The present sequence is a peptide tag
CC used to construct Zcytor16 mammalian expression vector
XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
|||
1 HHHHHH 6
Db 1 HHHHHH 6

Search completed: March 21, 2006, 11:04:21
Job time : 226 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:04:41 ; Search time 39 Seconds
(without alignments)
14.803 Million cell updates/sec

Title: US-10-719-523-5
Perfect score: 48
Sequence: 1 HHHHHH 6

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	48	100.0	16	1 LPECH	his operon leader
2	48	100.0	16	2 C90981	his operon leader
3	48	100.0	16	2 A85827	his operon leader
4	48	100.0	16	2 H64698	histidine and glut
5	48	100.0	60	2 C64698	probable histidine
6	48	100.0	64	2 S57787	hypothetical prote
7	48	100.0	77	2 D71821	probable histidine
8	48	100.0	77	2 T16436	hypothetical prote
9	48	100.0	83	2 T16435	hypothetical prote
10	48	100.0	92	2 T34146	hypothetical prote
11	48	100.0	101	2 B44971	hypothetical prote
12	48	100.0	102	2 T30119	hypothetical prote
13	48	100.0	114	2 S37150	asr2 protein - tom
14	48	100.0	115	2 H72583	hypothetical prote
15	48	100.0	122	2 T01558	auxin-induced prote
16	48	100.0	130	2 S14983	gene HOXA1 protein
17	48	100.0	132	2 S13193	extensin class I (
18	48	100.0	133	2 B10242	stem cell protein
19	48	100.0	136	2 T23959	hypothetical prote
20	48	100.0	139	2 T33968	hypothetical prote
21	48	100.0	140	2 T06554	histidine-rich pro
22	48	100.0	140	2 A54523	histidine-rich pro
23	48	100.0	140	2 T19083	hypothetical prote
24	48	100.0	141	2 T06553	probable profilin
25	48	100.0	143	1 B64421	conserved hypothet
26	48	100.0	172	2 T51065	hypothetical prote
27	48	100.0	176	2 T48265	hypothetical prote
28	48	100.0	180	2 B84774	probable RING zinc
29	48	100.0	192	2 T39367	hypothetical prote

30	48	100.0	206	2 T25384	hypothetical prote
31	48	100.0	208	2 T24446	hypothetical prote
32	48	100.0	216	2 T53100	ethAND - mouse
33	48	100.0	219	2 T32443	hypothetical prote
34	48	100.0	222	2 T39192	hypothetical prote
35	48	100.0	230	2 T47866	gene HOXA1 protein
36	48	100.0	235	2 D69101	regulatory protein
37	48	100.0	236	2 S41512	protein F25E5.8 (1
38	48	100.0	239	2 B66346	Brn-3b protein - m
39	48	100.0	255	2 S41511	FltF4.1 protein -
40	48	100.0	259	2 T51679	Brn-3a protein - m
41	48	100.0	259	2 A70359	myb-related trans
42	48	100.0	259	2 E66300	hydrogenase expres
43	48	100.0	268	2 A56446	Ig heavy chain V r
44	48	100.0	269	2 F96506	hypothetical prote
45	48	100.0	270	2 A26480	knob protein - mal
46	48	100.0	275	2 T02334	probable urease ac
47	48	100.0	285	2 B84766	probable At-hook D
48	48	100.0	290	2 T21868	hypothetical prote
49	48	100.0	292	2 T51171	transcription fact
50	48	100.0	294	2 E69759	hypothetical prote
51	48	100.0	295	2 B84747	hypothetical prote
52	48	100.0	297	2 S23737	proline-rich prote
53	48	100.0	298	2 S41469	homeotic protein M
54	48	100.0	302	2 A56641	homeotic protein G
55	48	100.0	303	2 B49122	homeobox protein M
56	48	100.0	303	2 A56837	homeotic protein M
57	48	100.0	303	2 A48130	growth arrest-spec
58	48	100.0	305	2 A65354	transcription fact
59	48	100.0	305	2 I57039	genomic screen hom
60	48	100.0	306	2 T09067	extensin-like prot
61	48	100.0	307	2 S38152	hypothetical prote
62	48	100.0	307	2 A45581	distal-less homeob
63	48	100.0	308	2 E70392	cation efflux syst
64	48	100.0	308	2 H89839	hypothetical prote
65	48	100.0	309	2 T29293	hypothetical prote
66	48	100.0	311	2 A56235	transcription acti
67	48	100.0	314	2 F96527	protein F27J15.20
68	48	100.0	315	2 J57572	sonite Maf1 protei
69	48	100.0	320	2 G83835	hypothetical prote
70	48	100.0	321	2 T02987	myb-related protei
71	48	100.0	323	2 I49529	transcription fact
72	48	100.0	323	2 T48160	transcription fact
73	48	100.0	323	2 I51751	homeotic protein o
74	48	100.0	324	2 B85064	MYB-like protein (
75	48	100.0	326	2 D83483	probable metal tra
76	48	100.0	328	2 S45998	hypothetical prote
77	48	100.0	328	2 G02469	homeotic protein D
78	48	100.0	331	2 S78452	POU-domain protein
79	48	100.0	331	2 A30242	homeotic protein E
80	48	100.0	332	2 JH0465	homeotic protein T
81	48	100.0	333	2 T52594	squamosa promoter
82	48	100.0	335	2 G01448	homeobox protein H
83	48	100.0	348	2 T04618	heat shock protein
84	48	100.0	349	2 E95858	conserved hypothet
85	48	100.0	349	2 AH2382	hypothetical prote
86	48	100.0	350	2 A30046	homeotic protein r
87	48	100.0	351	2 K8ZQHL	histidine-rich gly
88	48	100.0	351	2 T20270	hypothetical prote
89	48	100.0	354	2 S39406	homeotic protein o
90	48	100.0	355	2 S35345	oxl1 protein - mou
91	48	100.0	355	2 T56547	homeodomain protei
92	48	100.0	356	2 T48354	hypothetical prote
93	48	100.0	359	2 T21705	hypothetical prote
94	48	100.0	359	2 S14283	transcription fact
95	48	100.0	365	2 H87288	conserved hypothet
96	48	100.0	368	2 H96712	probable DNA-bindi
97	48	100.0	369	1 TVFVAR	transforming protei
98	48	100.0	370	2 T57555	c-Maf protein - mo
99	48	100.0	373	2 T52182	probable transcrip
100	48	100.0	374	2 H88503	protein B0361.4 (1
101	48	100.0	375	2 A46390	cAMP receptor subu
102	48	100.0	376	2 A49077	transcription init

103	48	100.0	379	2	S42543	hypothetical prote
104	48	100.0	380	2	S14188	carbonate dehydrat
105	48	100.0	385	1	OKRTP	selenoprotein P pr
106	48	100.0	385	2	A84696	probable zinc tra
107	48	100.0	385	2	T19201	hypothetical prote
108	48	100.0	387	2	A47446	HNf-3/Forx head fa
109	48	100.0	390	1	A38565	polycomb (Pc) prot
110	48	100.0	390	1	TVMVCB	transferring prote
111	48	100.0	391	2	A49645	transcription fact
112	48	100.0	391	2	H86187	hypothetical prote
113	48	100.0	391	2	H96572	protein F12M6.13
114	48	100.0	392	2	S11998	finger protein odd
115	48	100.0	401	2	S53405	probable membrane
116	48	100.0	404	2	D86321	hypothetical prote
117	48	100.0	404	2	T02396	hypothetical prote
118	48	100.0	407	2	G84783	probable pectinest
119	48	100.0	409	2	S60988	hypothetical prote
120	48	100.0	410	2	I38502	gene Bm-3b protei
121	48	100.0	411	2	I58156	Bm-3.2 - mouse
122	48	100.0	414	2	A40350	transcription repr
123	48	100.0	414	2	A48273	delta/Y1/NF-E1/UC
124	48	100.0	420	2	T19712	hypothetical prote
125	48	100.0	420	2	I59234	octamer binding tr
126	48	100.0	420	2	A49642	transcription fact
127	48	100.0	425	1	JH0710	transcription fact
128	48	100.0	427	2	T42516	hypothetical prote
129	48	100.0	430	2	S66671	neuron-derived rec
130	48	100.0	432	2	I51436	HNf-3/beta - Africa
131	48	100.0	439	2	T46375	hypothetical prote
132	48	100.0	444	2	T09474	forhead protein F
133	48	100.0	448	1	A56018	transcription fact
134	48	100.0	449	1	S30205	transcription fact
135	48	100.0	451	1	A40168	transcription fact
136	48	100.0	451	2	A55909	transforming prote
137	48	100.0	467	2	G84545	BHM transcription
138	48	100.0	467	2	T47773	hypothetical prote
139	48	100.0	469	2	I37451	HBf-G2 (HRK-2) pro
140	48	100.0	470	2	T20851	hypothetical prote
141	48	100.0	471	2	T33997	hypothetical prote
142	48	100.0	473	2	A54494	knob-associated hi
143	48	100.0	474	2	A40721	neuroblast prolif
144	48	100.0	476	2	S57963	methyl Gpg bindi
145	48	100.0	476	2	A54743	transcription fact
146	48	100.0	477	2	T47753	hypothetical prote
147	48	100.0	480	2	JH0672	brain factor 1 pro
148	48	100.0	490	2	S52830	HMS1 protein - Yea
149	48	100.0	492	2	A41907	methyl-Cpg-binding
150	48	100.0	495	1	S31223	transcription fact
151	48	100.0	496	2	S33791	ARS-binding protei
152	48	100.0	498	2	T13434	hypothetical prote
153	48	100.0	499	2	S09880	hypothetical prote
154	48	100.0	504	2	T33485	hypothetical prote
155	48	100.0	508	2	S59870	fork head domain p
156	48	100.0	510	2	T20850	hypothetical prote
157	48	100.0	525	2	F85227	hyc-Like protein
158	48	100.0	529	2	T00677	hypothetical prote
159	48	100.0	533	2	H86285	protein F10B6.34 (
160	48	100.0	549	1	S19095	transcription fact
161	48	100.0	550	2	T23760	hypothetical prote
162	48	100.0	550	2	S63641	hypothetical prote
163	48	100.0	559	2	T26141	hypothetical prote
164	48	100.0	564	2	T21983	hypothetical prote
165	48	100.0	568	2	S15008	gene disco protein
166	48	100.0	576	2	S69214	deformed epidermal
167	48	100.0	580	2	T46024	hypothetical prote
168	48	100.0	601	1	B56564	transcription fact
169	48	100.0	604	2	T00119	probable transcrip
170	48	100.0	604	2	S56027	hypothetical prote
171	48	100.0	606	2	A39369	homeotic protein B
172	48	100.0	606	2	S13367	Om(1D) protein - f
173	48	100.0	609	2	A49839	odd-paired - fruit
174	48	100.0	610	2	A57632	homeotic protein B
175	48	100.0	620	2	S52494	protein kinase hom
176	48	100.0	622	2	S71342	calnexin precursor
177	48	100.0	623	1	S33167	gene pointed prote
178	48	100.0	625	2	S71930	neuron-derived rec
179	48	100.0	628	2	JC2493	serine/threonine-s
180	48	100.0	633	1	A26030	histidine-rich pro
181	48	100.0	634	2	A28412	knob protein preu
182	48	100.0	634	2	A54495	BELL-like homeobox
183	48	100.0	638	2	D85435	knob-associated hi
184	48	100.0	654	2	B71623	knob-associated hi
185	48	100.0	657	2	A29454	hypothetical prote
186	48	100.0	661	2	T46364	lamin A - African
187	48	100.0	665	2	S02358	receptor-like prot
188	48	100.0	669	2	T07865	serum-inducible ki
189	48	100.0	682	2	A44493	hypothetical prote
190	48	100.0	688	2	T23108	SSV7 protein hom1
191	48	100.0	717	2	S38177	hypothetical prote
192	48	100.0	735	2	T45059	Down-syndrome-crit
193	48	100.0	754	2	JC4898	finger protein hum
194	48	100.0	758	2	A29253	hypothetical prote
195	48	100.0	766	2	T02702	hypothetical prote
196	48	100.0	776	2	S57702	probable peroxisom
197	48	100.0	791	2	T41573	hypothetical prote
198	48	100.0	802	2	T39171	gap protein hunchb
199	48	100.0	802	2	T33295	Cu2+-transporting
200	48	100.0	816	2	S05548	protein-tyrosine k
201	48	100.0	819	2	D85440	protein-tyrosine k
202	48	100.0	820	1	TWCTFR	protein-tyrosine k
203	48	100.0	820	2	I48347	Axin homolog Ax11
204	48	100.0	828	2	T08423	hypothetical prote
205	48	100.0	845	2	T17291	hypothetical prote
206	48	100.0	853	2	T46347	hypothetical prote
207	48	100.0	860	2	T23296	zinc finger bindi
208	48	100.0	895	2	JC7089	hypothetical prote
209	48	100.0	896	2	T51891	transforming prote
210	48	100.0	896	2	B43817	transforming prote
211	48	100.0	906	2	A43817	probable membrane
212	48	100.0	946	2	S48255	URSI1 protein - sm
213	48	100.0	950	2	S27473	DNA topoisomerase
214	48	100.0	972	2	S35521	hypothetical prote
215	48	100.0	991	2	C96764	hypothetical prote
216	48	100.0	1001	2	T28897	hypothetical prote
217	48	100.0	1019	2	T00117	dve protein - fruit
218	48	100.0	1057	2	T04874	hypothetical prote
219	48	100.0	1103	2	T26954	hypothetical prote
220	48	100.0	1116	2	S57382	hypothetical prote
221	48	100.0	1145	2	T33606	hypothetical prote
222	48	100.0	1166	2	T13958	synGAP-b1 protein
223	48	100.0	1172	2	F84572	probable cadmium-t
224	48	100.0	1172	2	T00065	hypothetical prote
225	48	100.0	1180	2	S69205	SH3-containing pro
226	48	100.0	1196	2	T14108	she protein - fruit
227	48	100.0	1212	2	T13804	hypothetical prote
228	48	100.0	1225	2	T16346	hypothetical prote
229	48	100.0	1245	2	T49815	related to multifu
230	48	100.0	1249	2	T14270	Rae-GTPase activat
231	48	100.0	1252	2	S36016	oocyte wall protei
232	48	100.0	1273	2	T00338	hypothetical prote
233	48	100.0	1291	2	T13389	hypothetical prote
234	48	100.0	1293	2	T14259	ras GTPase-activat
235	48	100.0	1305	2	A40879	phospholipase C (B
236	48	100.0	1312	1	B40879	phospholipase C (B
237	48	100.0	1338	2	T18287	protein-tyrosine k
238	48	100.0	1356	2	S51389	ROM2 protein - yea
239	48	100.0	1370	2	T19188	hypothetical prote
240	48	100.0	1398	2	T13741	hypothetical prote
241	48	100.0	1441	2	T13717	CRAG protein - fru
242	48	100.0	1465	2	T23056	chromodomain helic
243	48	100.0	1557	2	T13160	protein CNK - fruit
244	48	100.0	1560	2	T00080	hypothetical prote
245	48	100.0	1585	2	T31611	hypothetical prote
246	48	100.0	1597	1	BVFPSL	sol protein, large
247	48	100.0	1597	2	T08428	gene small optic l
248	48	100.0	1664	2	T18216	integrin-like prot

249	48	100.0	1753	2	S30855	hypothetical prote	322	41	85.4	1214	2	UC2069	zinc-finger protei
250	48	100.0	1785	2	T21558	hypothetical prote	323	41	85.4	1611	2	T38236	hypothetical prote
251	48	100.0	1820	2	T19430	hypothetical prote	324	40	83.3	82	2	A29653	histidine-rich pro
252	48	100.0	1887	2	C66478	protein F1504.13 l	325	40	83.3	102	2	AB2009	hypothetical prote
253	48	100.0	1929	2	T21559	hypothetical prote	326	40	83.3	107	2	A29995	probatine p2 precu
254	48	100.0	1958	2	B40505	hypothetical prote	327	40	83.3	113	2	S66936	probable membrane
255	48	100.0	2212	2	A41098	calcium channel pr	328	40	83.3	115	2	T06588	abscisic stress ri
256	48	100.0	2248	1	D42088	adenylate cyclase	329	40	83.3	117	2	T28394	hypothetical prote
257	48	100.0	2254	2	T09053	low voltage-activa	330	40	83.3	124	2	C72205	conserved hypothet
258	48	100.0	2273	2	I46477	calcium channel Bi	331	40	83.3	128	1	H69052	conserved hypothet
259	48	100.0	2326	2	B47447	calcium channel pr	332	40	83.3	130	2	F70585	probable furf prot
260	48	100.0	2396	2	T13714	kakapo gene protei	333	40	83.3	131	2	B53024	Leydig insulin-like
261	48	100.0	2436	2	T13825	adenomatous polyo	334	40	83.3	133	2	T45733	transcription regu
262	48	100.0	2424	2	I46480	calcium channel Bi	335	40	83.3	138	2	D83824	transcription regu
263	48	100.0	2429	2	T51023	hypothetical prote	336	40	83.3	138	2	T21299	hypothetical prote
264	48	100.0	3345	2	T13423	hypothetical prote	337	40	83.3	141	2	AE1255	transcription regu
265	48	100.0	3345	2	T30118	hypothetical prote	338	40	83.3	141	2	T46654	transcription regu
266	42	87.5	79	2	F84563	hypothetical prote	339	40	83.3	141	2	AB1618	transcription regu
267	42	87.5	244	2	A84687	probable homeodoma	340	40	83.3	145	2	H69954	transcription regu
268	42	87.5	271	2	JC6553	transcription fact	341	40	83.3	145	2	AE3531	zinc uptake regula
269	42	87.5	280	2	E96589	hypothetical prote	342	40	83.3	146	2	A95254	adc operon repres
270	42	87.5	309	2	G96782	hypothetical prote	343	40	83.3	146	2	T46753	repressor protein
271	42	87.5	319	2	T40156	sun family protein	344	40	83.3	147	2	T01039	hypothetical prote
272	42	87.5	370	2	T23553	hypothetical prote	345	40	83.3	148	2	G83681	urease accessory p
273	42	87.5	391	2	T18604	hypothetical prote	346	40	83.3	149	2	A54530	eggshell protein -
274	42	87.5	433	2	SS1773	transcription fact	347	40	83.3	151	2	AE2017	cell wall-binding
275	42	87.5	507	2	T49519	hypothetical prote	348	40	83.3	152	2	T51796	hypothetical prote
276	42	87.5	511	2	T26124	hypothetical prote	349	40	83.3	161	2	E43719	ureg protein - pro
277	42	87.5	638	2	B84799	similar to axl 1 p	350	40	83.3	165	2	S76947	hypothetical prote
278	42	87.5	661	2	T27016	hypothetical prote	351	40	83.3	166	2	G98118	hypothetical prote
279	42	87.5	680	2	T10656	probable ABC-type	352	40	83.3	169	2	T02081	ABA- and ripening-
280	42	87.5	723	2	I39066	N-methyl-D-asparta	353	40	83.3	188	2	H82933	hypothetical prote
281	42	87.5	824	2	I50618	C-fps proto onco	354	40	83.3	196	2	G85435	TINy-like protein
282	42	87.5	873	1	TVPF	protein-tyrosine k	355	40	83.3	207	2	H85070	hypothetical prote
283	42	87.5	1482	2	I49704	glutamate receptor	356	40	83.3	217	2	T06455	Myd26 protein - ga
284	42	87.5	1484	2	B43274	N-methyl-D-asparta	357	40	83.3	220	2	UC2337	T-cell receptor al
285	42	87.5	1484	2	SS2086	N-methyl-D-asparta	358	40	83.3	222	2	C48486	probable PRKG1-lik
286	42	87.5	1557	2	T02859	probable serine/th	359	40	83.3	235	2	S55883	CCHH finger protei
287	42	87.5	1839	1	OYBYK	adenylate cyclase	360	40	83.3	240	2	T45727	hypothetical prote
288	42	87.5	1941	2	T23979	hypothetical prote	361	40	83.3	245	2	T23153	hypothetical prote
289	42	87.5	1943	2	T23986	hypothetical prote	362	40	83.3	251	2	T06387	knotted I class ho
290	41	85.4	66	2	T06697	hypothetical prote	363	40	83.3	259	2	T52619	TINy-like protein
291	41	85.4	134	2	S71249	embryonic protein	364	40	83.3	262	2	B82120	zinc ABC transport
292	41	85.4	136	2	A89936	hypothetical prote	365	40	83.3	264	2	T52104	GATrABC binding trans
293	41	85.4	140	2	T27059	hypothetical prote	366	40	83.3	265	2	T49008	hypothetical prote
294	41	85.4	143	2	S66340	phloem-specific pr	367	40	83.3	270	2	S74993	hypothetical prote
295	41	85.4	197	2	AE1154	methyltransferase	368	40	83.3	274	2	T29574	hypothetical prote
296	41	85.4	199	2	A11512	weakly methyltrans	369	40	83.3	276	2	A64978	hypothetical prote
297	41	85.4	268	2	B64066	probable ABC trans	370	40	83.3	277	2	T29894	hypothetical prote
298	41	85.4	281	2	AB1894	hydrogenase expres	371	40	83.3	279	2	S54157	extensin-like prot
299	41	85.4	306	2	S59540	heat shock transcr	372	40	83.3	279	2	H80992	hypothetical prote
300	41	85.4	329	2	T45972	hypothetical prote	373	40	83.3	283	2	C65838	hypothetical prote
301	41	85.4	335	2	T34086	hypothetical prote	374	40	83.3	285	2	S75853	hypothetical prote
302	41	85.4	356	2	T06756	hypothetical prote	375	40	83.3	292	2	T00829	muschel protein -
303	41	85.4	368	2	S46727	hypothetical prote	376	40	83.3	293	2	T05153	hypothetical prote
304	41	85.4	368	2	G86636	protein W09G12.7 l	377	40	83.3	293	2	D84558	probable homeodoma
305	41	85.4	370	2	S59539	heat shock transcr	378	40	83.3	298	2	H84795	probable MYB famli
306	41	85.4	371	2	F85434	geranylgeranyl pyr	379	40	83.3	298	2	AE3531	high-affinity zinc
307	41	85.4	386	2	T09598	cyclin 4, D-type -	380	40	83.3	302	2	A87369	copper-binding pro
308	41	85.4	551	2	T49922	pectin methyl ester	381	40	83.3	303	2	H97212	co/Zn/Cd efflux sy
309	41	85.4	590	2	T01237	hypothetical prote	382	40	83.3	303	2	S23440	hypothetical prote
310	41	85.4	632	2	T32454	hypothetical prote	383	40	83.3	306	2	T44684	hypothetical prote
311	41	85.4	658	2	T04219	hypothetical prote	384	40	83.3	306	2	A88040	protein P47F6.1 li
312	41	85.4	669	2	S14535	asparagine-rich pr	385	40	83.3	312	2	A10138	probable cation tr
313	41	85.4	762	2	C96653	hypothetical prote	386	40	83.3	315	2	T50561	SINA1 protein (amp
314	41	85.4	828	2	C88402	protein H05C05.1 l	387	40	83.3	317	2	AH0351	hypothetical prote
315	41	85.4	887	1	IUCHCL	E-cadherin precurs	388	40	83.3	324	2	T22580	hypothetical prote
316	41	85.4	1028	2	A56038	DNA-binding protei	389	40	83.3	326	2	B84812	hypothetical prote
317	41	85.4	1036	1	A34755	nitrogen regulator	390	40	83.3	328	2	AH3531	high-affinity zinc
318	41	85.4	1046	2	S67786	hypothetical prote	391	40	83.3	329	2	D82449	conserved hypothet
319	41	85.4	1087	2	T49496	hypothetical prote	392	40	83.3	330	2	T05717	probable extensin
320	41	85.4	1198	2	T42223	ladder protein - C	393	40	83.3	331	1	S69190	myb-related protei
321	41	85.4	1213	2	S16356	ovo protein - fru1	394	40	83.3	334	2	H96791	unknown protein Fl

395	40	83.3	341	2	E83340	hypothetical prote
396	40	83.3	341	2	T51957	metalloproteinase
397	40	83.3	342	2	G84885	hypothetical prote
398	40	83.3	343	2	T29547	hypothetical prote
399	40	83.3	353	2	A82396	hypothetical prote
400	40	83.3	360	2	T04535	hypothetical prote
401	40	83.3	361	2	B84716	hypothetical prote
402	40	83.3	361	2	J02379	homeobox 1 protein
403	40	83.3	364	2	T02801	probable membrane
404	40	83.3	374	2	AB1943	hypothetical prote
405	40	83.3	377	2	A35795	carbonate dehydrat
406	40	83.3	380	2	T10442	selenoprotein P pr
407	40	83.3	380	2	H83994	hypothetical prote
408	40	83.3	381	1	A47327	selenoprotein P pr
409	40	83.3	383	2	S76964	hypothetical prote
410	40	83.3	388	2	AC3256	cobw protein limpo
411	40	83.3	395	2	SA3344	sex-determining pr
412	40	83.3	395	2	S35565	sex-determining pr
413	40	83.3	398	2	T02681	probable zinc tran
414	40	83.3	402	2	A72312	conserved hypotet
415	40	83.3	408	2	P85023	probable potassium
416	40	83.3	411	2	AC3003	conserved hypotet
417	40	83.3	411	2	B98280	hypothetical prote
418	40	83.3	415	2	B84858	hypothetical prote
419	40	83.3	416	2	T31486	hypothetical prote
420	40	83.3	419	1	WJFFH2	homeotic protein H
421	40	83.3	426	2	AH1831	hypothetical prote
422	40	83.3	426	2	A26330	hypothetical prote
423	40	83.3	427	2	A32372	female-specific do
424	40	83.3	427	2	T04869	transforming prote
425	40	83.3	430	2	T04678	hypothetical prote
426	40	83.3	439	2	P86592	probable zinc fing
427	40	83.3	461	2	S34472	Mpf-1 protein - mo
428	40	83.3	462	2	C84473	probable protein k
429	40	83.3	466	2	A88868	protein T2385.3 [i
430	40	83.3	471	2	S41768	splicing factor ho
431	40	83.3	471	2	G01211	54 kDa protein - h
432	40	83.3	472	2	A26357	homeotic protein C
433	40	83.3	473	2	T04225	hypothetical prote
434	40	83.3	473	2	AS4691	occamer-binding pr
435	40	83.3	490	2	T25147	hypothetical prote
436	40	83.3	491	2	H84840	hypothetical prote
437	40	83.3	493	2	C86390	amino acid transpo
438	40	83.3	496	2	S52421	hypothetical prote
439	40	83.3	506	2	T33496	hypothetical prote
440	40	83.3	506	2	A86169	hypothetical prote
441	40	83.3	507	2	C71412	probable hydroxypr
442	40	83.3	510	2	A33380	nuclear protein fx
443	40	83.3	513	2	S69181	protein disulfide-
444	40	83.3	515	1	T38946	phosphoprotein pho
445	40	83.3	516	2	T01419	cellulase (BC 3.2.
446	40	83.3	529	2	H81650	conserved hypotet
447	40	83.3	531	2	H72040	conserved hypotet
448	40	83.3	531	2	G86583	CT632 hypothetical
449	40	83.3	532	2	T07903	tubulin delta chai
450	40	83.3	539	2	B32372	male-specific doub
451	40	83.3	571	2	T01511	hypothetical prote
452	40	83.3	571	2	D96516	Fl633.14 limported
453	40	83.3	576	2	A26628	homeotic protein I
454	40	83.3	586	2	T04716	hypothetical prote
455	40	83.3	602	2	P84432	probable C2H2-type
456	40	83.3	612	2	AS4282	reversed polarity
457	40	83.3	624	2	T05090	hypothetical prote
458	40	83.3	640	2	A41726	homeotic protein B
459	40	83.3	642	2	S27806	homeotic protein B
460	40	83.3	654	2	T08600	hypothetical prote
461	40	83.3	657	2	S05517	lamn - chicken
462	40	83.3	661	2	F83342	probable cation-tr
463	40	83.3	699	2	AS4660	histidine rich cal
464	40	83.3	719	2	C88216	protein B0495.2 [i
465	40	83.3	752	2	G03273	liv-1 protein - hu
466	40	83.3	759	2	S67164	probable membrane
467	40	83.3	808	2	T51232	scarecrow-like pro
468	40	83.3	822	1	TVHUF	protein-tyrosine k
469	40	83.3	839	1	TQ2MCA	probable transposa
470	40	83.3	841	1	S2462	probable 3',5'-cyc
471	40	83.3	880	2	S56828	finger protein ydl
472	40	83.3	884	1	ITMSCR	E-cadherin precurs
473	40	83.3	884	2	S34438	uvomoulin - mouse
474	40	83.3	918	2	D88544	protein R08D7.6 [i
475	40	83.3	960	2	G84652	probable receptor
476	40	83.3	963	2	T48707	related to regulat
477	40	83.3	971	2	T4866	hypothetical prote
478	40	83.3	1014	2	T13476	hypothetical prote
479	40	83.3	1040	2	T29092	Tsc-22 protein hom
480	40	83.3	1057	2	T25396	hypothetical prote
481	40	83.3	1090	2	A41696	regulatory protein
482	40	83.3	1184	2	S50832	atrophin-1 - human
483	40	83.3	1184	2	G01763	atrophin-1 - human
484	40	83.3	1201	2	G86441	unknown protein [i
485	40	83.3	1246	2	T51085	related to protein
486	40	83.3	1299	1	S06119	membrane protein p
487	40	83.3	1307	2	G36711	unknown protein, 9
488	40	83.3	1398	2	S56814	microtubule-intera
489	40	83.3	1541	2	T02831	AAA protein L4171.
490	40	83.3	1557	2	T18412	lipid-binding prote
491	40	83.3	2163	2	T15276	hypothetical prote
492	40	83.3	2237	2	T51125	N-type calcium cha
493	40	83.3	2288	2	S41080	calcium channel al
494	40	83.3	2336	2	A45386	omega-conotoxin-se
495	40	83.3	2339	2	A42566	hypothetical prote
496	40	83.3	2342	2	T13412	hypothetical prote
497	39	81.2	143	2	A86819	hypothetical prote
498	39	81.2	167	2	B83034	urase accessory p
499	39	81.2	191	2	AD2871	urase accessory p
500	39	81.2	196	2	T26943	hypothetical prote
501	39	81.2	198	2	E86261	FlXk23.6 protein -
502	39	81.2	201	2	AH3332	urase accessory p
503	39	81.2	222	2	P97647	urase accessory p
504	39	81.2	247	2	P81410	hydrogenase isoenz
505	39	81.2	248	2	D96535	RING-H2 finger pro
506	39	81.2	251	2	F64745	probable hydroxyac
507	39	81.2	251	2	H90654	probable hydroxyac
508	39	81.2	251	2	H85505	probable hydroxyac
509	39	81.2	252	2	A82102	probable hydroxyac
510	39	81.2	258	2	G83417	probable hydroxyac
511	39	81.2	269	2	B82959	zinc transport pro
512	39	81.2	275	2	T52333	urase accessory p
513	39	81.2	305	2	JN0647	hydrogenase expres
514	39	81.2	310	2	T00609	hypothetical prote
515	39	81.2	311	2	B85577	probable transport
516	39	81.2	312	2	A86279	Fl417.21 protein
517	39	81.2	313	1	H64810	ybgr protein - Sac
518	39	81.2	313	2	D90726	probable transport
519	39	81.2	332	2	C83682	hypothetical prote
520	39	81.2	335	2	T47235	sex determining pr
521	39	81.2	356	2	T43145	hypothetical prote
522	39	81.2	372	2	AC3548	low affinity zinc
523	39	81.2	374	2	A96798	hypothetical prote
524	39	81.2	375	2	AB3110	conserved hypotet
525	39	81.2	375	2	B98177	hypothetical prote
526	39	81.2	434	2	C96515	hypothetical prote
527	39	81.2	444	2	P96835	hypothetical prote
528	39	81.2	458	2	B39533	transcription fact
529	39	81.2	459	1	B42558	transcription fact
530	39	81.2	466	2	S19365	hypothetical prote
531	39	81.2	477	2	T29592	hypothetical prote
532	39	81.2	509	2	A53741	transcription fact
533	39	81.2	537	2	JH0415	synapogamin o-p65
534	39	81.2	617	2	A90644	probable membrane
535	39	81.2	617	2	AS5495	probable membrane
536	39	81.2	617	2	B64734	yach protein - Sac
537	39	81.2	617	2	T23197	hypothetical prote
538	39	81.2	623	2	T28958	hypothetical prote
539	39	81.2	642	2	T45904	protein kinase-1lk
540	39	81.2	648	2	T47896	hypothetical prote

541	39	81.2	1016	1	A46079	protein kinase C (614	37	77.1	315	2	T04624	hypothetical prote
542	39	81.2	2026	1	OXYB	adenylate cyclase	615	37	77.1	356	2	G84904	probable DOF zinc
543	39	81.2	2167	2	S50658	bud emergence prot	616	37	77.1	389	2	C96830	unknown protein P1
544	39	81.2	3119	2	T18414	protein g377 - mal	617	37	77.1	429	2	S01919	knirps protein - f
545	38	79.2				hypothetical prote	618	37	77.1	431	2	T51266	hypothetical prote
546	38	79.2	86	2	T16437	hypothetical 11.6k	619	37	77.1	432	2	B96515	hypothetical prote
547	38	79.2	116	2	T46320	hypothetical prote	620	37	77.1	433	2	C97682	probable intracell
548	38	79.2	147	2	T16440	hypothetical prote	621	37	77.1	443	2	B84449	hypothetical prote
549	38	79.2	158	2	D16138	urea protein - xle	622	37	77.1	477	2	T45722	hypothetical prote
550	38	79.2	160	2	A81075	PKB-type peptidyl	623	37	77.1	523	2	S67271	hypothetical prote
551	38	79.2	199	2	T48099	hypothetical prote	624	37	77.1	529	2	T08684	hypothetical prote
552	38	79.2	273	2	T49442	hypothetical prote	625	37	77.1	597	2	T23961	hypothetical prote
553	38	79.2	290	2	T49631	probable Ni-bindin	626	37	77.1	637	2	S66953	hypothetical prote
554	38	79.2	295	2	B48013	proline-rich prote	627	37	77.1	643	2	T27429	hypothetical prote
555	38	79.2	297	2	A35874	myogenic factor 1	628	37	77.1	798	2	S20881	hypothetical prote
556	38	79.2	299	2	S32874	hydp protein - Rhi	629	37	77.1	832	2	T08422	hypothetical prote
557	38	79.2	303	2	AG1396	cation transport p	630	37	77.1	834	2	UC7993	ary1 hydriocarbon r
558	38	79.2	303	2	AB1772	cation transport p	631	37	77.1	883	2	T33656	hypothetical prote
559	38	79.2	311	2	A53808	homeotic protein c	632	37	77.1	901	2	UC6093	dead ringier nuclea
560	38	79.2	313	2	A46233	FLAT element-bind	633	37	77.1	982	2	T19526	hypothetical prote
561	38	79.2	325	2	T44365	cation-efflux svst	634	37	77.1	1733	1	B45344	probable nuclear a
562	38	79.2	325	2	G90008	hypothetical prote	635	37	77.1	1762	2	T03222	probable polykeid
563	38	79.2	335	2	T52249	probable basic hel	636	37	77.1	2101	2	S57245	insulin receptor (
564	38	79.2	336	1	S75947	hypothetical prote	637	37	77.1	2148	1	A56081	insulin receptor -
565	38	79.2	338	2	T36785	hypothetical prote	638	37	76.0	237	2	T09848	H+-exporting ATPas
566	38	79.2	346	2	AH1189	B. subtilis ycgR p	639	36.5	76.0	346	2	T32585	hypothetical prote
567	38	79.2	349	2	AT1547	B. subtilis ycgR p	640	36.5	76.0	368	2	T32587	hypothetical prote
568	38	79.2	349	2	A56365	slk gland factor-	641	36.5	76.0	482	2	S22654	ARS-binding factor
569	38	79.2	359	2	B86409	F3H9.6 protein - A	642	36.5	76.0	540	2	AD0522	probable exported
570	38	79.2	361	2	F87286	cation efflux faml	643	36.5	76.0	813	2	AH3258	cation-transportin
571	38	79.2	380	2	UQ2338	omega-3 fatty acid	644	36.5	76.0	828	2	T06133	hypothetical prote
572	38	79.2	405	2	T21188	hypothetical prote	645	36.5	76.0	974	1	A40213	optic lobe develop
573	38	79.2	410	2	T26757	hypothetical prote	646	36.5	76.0	1429	2	T13720	gene expanded prot
574	38	79.2	470	2	S33639	finger protein esc	647	36	75.0	173	2	T51469	glycine/proline-ri
575	38	79.2	482	2	E84680	probable glucosylt	648	36	75.0	240	2	T45724	hypothetical prote
576	38	79.2	491	2	A32584	Abd-B protein - fr	649	36	75.0	261	2	T18320	hypothetical prote
577	38	79.2	493	2	A34220	homeotic protein A	650	36	75.0	271	2	B83027	thiosulfate sulfur
578	38	79.2	572	2	T34658	hypothetical prote	651	36	75.0	415	2	T13651	hypothetical prote
579	38	79.2	577	2	T16333	hypothetical prote	652	36	75.0	430	2	C68346	hypothetical prote
580	38	79.2	594	2	UC5146	ary1phorin gene-sp	653	36	75.0	1819	2	T32008	hypothetical prote
581	38	79.2	629	2	A30168	homeotic protein L	654	35.5	74.0	118	1	A31429	hhaecophillin [val
582	38	79.2	632	2	S44917	ZK688.2 protein -	655	35.5	74.0	184	2	S35751	1ox10 protein - 1e
583	38	79.2	635	2	S01164	homeotic protein L	656	35.5	74.0	1851	2	T19964	hypothetical prote
584	38	79.2	670	1	S50591	myb-related protei	657	35	72.9	144	2	F71446	hypothetical prote
585	38	79.2	688	2	T09941	transcription fact	658	35	72.9	161	2	T25483	hypothetical prote
586	38	79.2	731	1	UC2464	probable copper-tr	659	35	72.9	224	2	T14474	MADS box protein a
587	38	79.2	732	2	T08420	1-phosphatidylinos	660	35	72.9	224	2	T14473	MADS box protein 2
588	38	79.2	743	2	T02828	conserved hypotet	661	35	72.9	268	2	C90056	conserved hypotet
589	38	79.2	894	2	F84870	hypothetical prote	662	35	72.9	316	2	T19435	hypothetical prote
590	38	79.2	943	2	T03306	PSD-95/SAP90-asso	663	35	72.9	445	2	S23055	SLP2 protein - fru
591	38	79.2	1008	2	T41244	SRG14 protein homo	664	35	72.9	445	2	S23056	SLP2 protein - fru
592	38	79.2	1241	2	S01827	petrid clock prote	665	35	72.9	459	2	D86315	hypothetical prote
593	38	79.2	1257	2	S28764	neurocan precursr	666	35	72.9	542	2	H86239	hypothetical prote
594	38	79.2	1268	2	S52781	neurocan - mouse	667	35	72.9	546	2	S29522	hypothetical prote
595	38	79.2	1355	2	S40022	spalt protein - fr	668	35	72.9	553	2	T27245	casein kinase I ho
596	38	79.2	2175	1	S03170	homeotic protein c	669	35	72.9	568	2	H88904	hypothetical prote
597	37.5	78.1	320	2	A96570	NAM-like protein.	670	35	72.9	624	2	T26148	hypothetical prote
598	37.5	78.1	324	2	F96588	hypothetical prote	671	35	72.9	659	2	T27246	hypothetical prote
599	37.5	78.1	694	2	S71786	wingless receptor	672	35	72.9	1615	2	B49502	protein-tyrosine-p
600	37.5	78.1	2559	2	T09144	probable guanine n	673	35	72.9	1767	2	A49502	protein-tyrosine-p
601	37	77.1	47	2	E81833	hypothetical prote	674	34.5	71.9	1969	2	T08875	histidine kinase h
602	37	77.1	126	2	T09789	abscisic acid- and	675	34	70.8	87	2	C84494	hypothetical prote
603	37	77.1	126	2	T15993	abscisic acid- and	676	34	70.8	90	2	D71568	hypothetical prote
604	37	77.1	136	2	T02663	abscisic acid- and	677	34	70.8	98	2	G82826	hypothetical prote
605	37	77.1	143	2	T12245	ABA stress-rilpen	678	34	70.8	107	2	H82365	conserved hypotet
606	37	77.1	153	2	T09832	water-stress-induc	679	34	70.8	150	2	I48670	gene ms22 protein
607	37	77.1	170	2	A22937	transforming prote	680	34	70.8	158	2	T46139	hypothetical prote
608	37	77.1	195	2	H96586	hypothetical prote	681	34	70.8	176	2	C90271	conserved hypotet
609	37	77.1	228	2	T07066	MADS-box protein h	682	34	70.8	179	2	G96001	conserved hypotet
610	37	77.1	228	2	T07410	MADS box protein h	683	34	70.8	185	2	H84601	probable dehydrin
611	37	77.1	231	2	S31693	MADS box protein g	684	34	70.8	196	2	G89907	hypothetical prote
612	37	77.1	278	2	E87704	hypothetical prote	685	34	70.8	199	2	C96681	hypothetical prote
613	37	77.1	285	2	I51412	hypothetical trans	686	34	70.8	208	2	T52368	homeobox protein H

687	34	70.8	217	2	T02548	hypothetical prote	760	34	70.8	790	2	T12203	transcription fact
688	34	70.8	217	2	T48642	hypothetical prote	761	34	70.8	857	2	T04208	probable anthranil
689	34	70.8	228	2	S55888	CCHH finger protei	762	34	70.8	873	1	TWFE5	protein-tyrosine k
690	34	70.8	235	2	B84967	hypothetical prote	763	34	70.8	952	2	D86179	hypothetical prote
691	34	70.8	245	2	T07139	cytosine proteins	764	34	70.8	1032	2	F55071	hypothetical prote
692	34	70.8	249	2	T21920	hypothetical prote	765	34	70.8	1032	2	C85943	probable oxidoredu
693	34	70.8	257	2	A84848	probable C2H2-type	766	34	70.8	1032	2	G91097	probable oxidoredu
694	34	70.8	265	2	T47898	hypothetical prote	767	34	70.8	1048	2	C96669	protein FIN19.15 f
695	34	70.8	280	2	A39484	androgen-wiltdrawa	768	34	70.8	1129	2	T19779	hypothetical prote
696	34	70.8	280	2	T24454	hypothetical prote	769	34	70.8	1146	2	S46837	hypothetical prote
697	34	70.8	283	2	JC4256	hypothetical 32.0k	770	34	70.8	1240	2	S52734	hypothetical prote
698	34	70.8	291	2	S33209	extensin-like prot	771	34	70.8	1256	2	S14556	asparagine-rich pr
699	34	70.8	302	2	H96811	protein F3F9.20 f1	772	34	70.8	1325	2	T25753	hypothetical prote
700	34	70.8	304	2	D81182	adhesin, probable	773	34	70.8	1407	2	B42239	adenylate cyclase
701	34	70.8	307	2	S37252	homeotic protein H	774	34	70.8	1671	2	S71628	hypothetical prote
702	34	70.8	308	2	T06218	catalase (EC 1.11.	775	34	70.8	1966	2	T32552	hypothetical prote
703	34	70.8	314	2	D71410	hypothetical prote	776	34	70.8	2161	2	JH0564	calcium channel al
704	34	70.8	315	2	C96666	protein F22C12.4 l	777	34	70.8	2181	2	A38198	calcium channel al
705	34	70.8	316	2	B84636	NAM (no apical mer	778	34	70.8	2203	2	T12742	voltage-dependent
706	34	70.8	322	2	S23053	slippy paired prot	779	34	70.8	2848	2	T32550	hypothetical prote
707	34	70.8	348	2	T06385	probable Fe(II) tr	780	33.5	69.8	183	2	C85439	probable cytoskele
708	34	70.8	349	2	S61414	DNA-binding protei	781	33.5	69.8	438	2	B84922	hypothetical prote
709	34	70.8	351	2	T03946	kn1 like-homo box	782	33.5	69.8	992	1	GNMVR3	structural polypor
710	34	70.8	352	2	T23464	hypothetical prote	783	33.5	69.8	1063	1	GNMVR7	structural polypor
711	34	70.8	362	2	T48564	probable serine ri	784	33.5	69.8	1063	1	GNMVR4	structural polypor
712	34	70.8	398	2	C84780	hypothetical prote	785	33.5	69.8	1063	1	GNMVR4	structural polypor
713	34	70.8	400	2	T25889	hypothetical prote	786	33.5	69.8	1291	2	T00019	period protein hom
714	34	70.8	401	2	T48495	hypothetical prote	787	33	68.8	84	2	AD2158	hypothetical prote
715	34	70.8	407	2	T08965	hypothetical prote	788	33	68.8	96	2	T46181	hypothetical prote
716	34	70.8	439	2	A84431	probable C2H2-type	789	33	68.8	121	2	A84906	probable auxin-reg
717	34	70.8	441	2	S50112	nuclear factor 1-X	790	33	68.8	122	2	C53234	glutulin-10 - maiz
718	34	70.8	441	2	B31256	transcription fact	791	33	68.8	136	2	AD2898	ATP synthase eps11
719	34	70.8	442	2	E71523	conserved hypotet	792	33	68.8	136	2	E97673	ATP synthase eps11
720	34	70.8	446	2	B82975	conserved hypotet	793	33	68.8	140	2	T16574	hypothetical prote
721	34	70.8	465	2	T18793	hypothetical prote	794	33	68.8	150	2	A84488	hypothetical prote
722	34	70.8	471	2	A81680	conserved hypotet	795	33	68.8	152	2	D75485	conserved hypotet
723	34	70.8	472	2	T18801	hypothetical prote	796	33	68.8	152	2	F84642	hypothetical prote
724	34	70.8	488	2	A55180	homeotic protein H	797	33	68.8	158	2	AF2476	hypothetical prote
725	34	70.8	490	2	A46391	CAMP receptor subc	798	33	68.8	176	2	A86441	hypothetical prote
726	34	70.8	492	1	CS8Y	catalase (EC 1.11.	799	33	68.8	179	2	T49508	hypothetical prote
727	34	70.8	492	2	S71112	catalase (EC 1.11.	800	33	68.8	180	2	B97242	embryonic abundant
728	34	70.8	492	2	T15969	catalase (EC 1.11.	801	33	68.8	184	2	S32095	hypothetical prote
729	34	70.8	492	2	S62696	catalase (EC 1.11.	802	33	68.8	184	2	A85036	hypothetical prote
730	34	70.8	492	2	S48124	catalase (EC 1.11.	803	33	68.8	187	2	T50832	hypothetical prote
731	34	70.8	492	2	S10770	catalase (EC 1.11.	804	33	68.8	190	2	D64087	probable peptidylp
732	34	70.8	492	2	S17493	catalase (EC 1.11.	805	33	68.8	205	2	T18811	probable chloride
733	34	70.8	492	2	S10395	catalase (EC 1.11.	806	33	68.8	207	2	B71445	hypothetical prote
734	34	70.8	492	2	T08754	catalase (EC 1.11.	807	33	68.8	215	2	S28062	homeotic protein g
735	34	70.8	492	2	T08756	catalase (EC 1.11.	808	33	68.8	219	2	H84584	hypothetical prote
736	34	70.8	492	2	T05779	catalase (EC 1.11.	809	33	68.8	224	2	T49923	hypothetical prote
737	34	70.8	492	2	S46297	catalase (EC 1.11.	810	33	68.8	228	2	S03639	superoxide dismuta
738	34	70.8	492	2	T10902	catalase (EC 1.11.	811	33	68.8	229	2	T50828	superoxide dismuta
739	34	70.8	493	2	T07911	catalase (EC 1.11.	812	33	68.8	229	2	AC0698	probable pathogeni
740	34	70.8	494	1	CS8M	catalase (EC 1.11.	813	33	68.8	232	2	A42095	floral homeotic pr
741	34	70.8	507	2	B96590	hypothetical prote	814	33	68.8	236	2	T01662	glutulin-1 - maiz
742	34	70.8	518	1	NIBCRT	nitrogenase (EC 1.	815	33	68.8	240	2	A37004	outer membrane cla
743	34	70.8	521	2	S27475	nitrogenase (EC 1.	816	33	68.8	242	2	A81782	outer membrane pro
744	34	70.8	529	2	D71489	hypothetical prote	817	33	68.8	242	2	C81205	outer membrane pro
745	34	70.8	531	2	T04722	hypothetical prote	818	33	68.8	244	2	F68830	conserved hypotet
746	34	70.8	537	2	T34380	hypothetical prote	819	33	68.8	251	2	AC0534	probable hydroxyc
747	34	70.8	566	2	S54629	hypothetical prote	820	33	68.8	251	2	T52370	homeobox protein H
748	34	70.8	575	2	T01552	hypothetical prote	821	33	68.8	251	2	T49950	homeobox-leucine z
749	34	70.8	587	2	A56015	finger protein SIG	822	33	68.8	251	2	H90949	hypothetical prote
750	34	70.8	615	2	T06108	hypothetical prote	823	33	68.8	251	2	D85798	hypothetical prote
751	34	70.8	627	2	T00600	hypothetical prote	824	33	68.8	251	2	B64948	probable ABC trans
752	34	70.8	633	2	T14612	hypothetical prote	825	33	68.8	251	2	AH0742	high-affinity zinc
753	34	70.8	650	2	T02536	CER1-like protein	826	33	68.8	256	2	T39108	probable hydroxyc
754	34	70.8	650	2	S44806	Om(2D) protein - f	827	33	68.8	260	2	T26496	hypothetical prote
755	34	70.8	671	2	S51599	GI cyclin C1N1 - Y	828	33	68.8	274	2	S70130	hypothetical prote
756	34	70.8	698	2	S49206	malate synthase BH	829	33	68.8	281	2	T15980	hypothetical prote
757	34	70.8	727	2	B83916	DNA-binding protei	830	33	68.8	285	2	S62179	hypothetical prote
758	34	70.8	731	2	S2870	probable GCNA-comp	831	33	68.8	300	2	T38966	hypothetical prote
759	34	70.8	776	2	A96634		832	33	68.8	303	2	G85062	

833	33	68.8	313	2	T01587	hypothetical prote	906	32	66.7	102	2	AE1795	PTS cellobiose-spe
834	33	68.8	318	2	T06322	anexin, isoform P	907	32	66.7	102	2	S09828	hypothetical prote
835	33	68.8	315	2	AB0251	excreted high-affi	908	32	66.7	104	2	S57666	protamine 2 - rat
836	33	68.8	323	2	T45601	hypothetical prote	909	32	66.7	106	2	T17663	hypothetical prote
837	33	68.8	324	2	F84719	probable glyoxalas	910	32	66.7	106	2	C17094	hypothetical prote
838	33	68.8	325	2	T04677	hypothetical prote	911	32	66.7	107	2	A69547	conserved hypotnet
839	33	68.8	325	2	G96718	unknown protein, 5	912	32	66.7	111	2	C35826	hypothetical 13K p
840	33	68.8	336	2	F85021	probable transcrip	913	32	66.7	112	2	T34857	hypothetical prote
841	33	68.8	347	2	S43771	phosphatidylcholin	914	32	66.7	115	2	A23925	proline-rich phosp
842	33	68.8	348	2	T02006	transcription fact	915	32	66.7	126	2	T52525	tyrosinase co-fact
843	33	68.8	350	2	S43772	phosphatidylcholin	916	32	66.7	131	2	B87012	probable ferric up
844	33	68.8	350	2	AH2005	phosphatidylcholin	917	32	66.7	131	2	A53024	Leydig insulin-lik
845	33	68.8	352	2	T15981	hypothetical prote	918	32	66.7	132	2	C75466	probable ferric up
846	33	68.8	357	2	F70193	hypothetical prote	919	32	66.7	133	2	AB0990	nickel responsive
847	33	68.8	364	2	T24966	hypothetical prote	920	32	66.7	133	2	D86018	nickel-responsive
848	33	68.8	367	2	T25093	hypothetical prote	921	32	66.7	133	2	D91172	nickel-responsive
849	33	68.8	367	2	D97096	probable permease,	922	32	66.7	133	2	S47700	nickel-responsive
850	33	68.8	369	2	T48612	hypothetical prote	923	32	66.7	134	2	A26986	hypothetical prote
851	33	68.8	376	1	Q08EW2	UL53 protein - hum	924	32	66.7	139	2	B33910	sal homeotic prote
852	33	68.8	381	2	T24290	hypothetical prote	925	32	66.7	139	2	T20162	hypothetical prote
853	33	68.8	383	2	T06753	hypothetical prote	926	32	66.7	142	2	S00262	sal homeotic prote
854	33	68.8	397	2	S54018	DBP2 protein-inter	927	32	66.7	142	2	C33910	hypothetical prote
855	33	68.8	398	2	D85080	KNAT1 homeobox-11k	928	32	66.7	146	2	H37788	hypothetical prote
856	33	68.8	405	2	D96709	probable B-box zin	929	32	66.7	146	2	C96708	hypothetical prote
857	33	68.8	407	2	T02258	globulin1 - maize	930	32	66.7	147	2	T52015	hypothetical prote
858	33	68.8	413	2	H81659	branched-chain ami	931	32	66.7	149	2	B82894	hypothetical prote
859	33	68.8	424	2	JC5891	omega 6 desaturase	932	32	66.7	150	2	C71706	hypothetical prote
860	33	68.8	445	2	A60488	histidine-rich gly	933	32	66.7	151	2	A53570	nickel-responsive
861	33	68.8	457	2	T21063	hypothetical prote	934	32	66.7	151	2	B37107	ferric uptake regu
862	33	68.8	506	2	JC7226	endo-1,3(4)-beta-g	935	32	66.7	154	2	B87029	hypothetical prote
863	33	68.8	512	2	F86196	hypothetical prote	936	32	66.7	155	2	JC7732	trypsin-plasmin in
864	33	68.8	524	2	F96572	protein F12M16.10	937	32	66.7	156	2	B85814	DNA mismatch endon
865	33	68.8	530	2	T50498	myc-like protein -	938	32	66.7	156	2	B90966	DNA mismatch endon
866	33	68.8	538	1	S12570	homeotic protein b	939	32	66.7	156	2	AC0754	patch repair prote
867	33	68.8	540	2	S21825	vicilin-like stora	940	32	66.7	156	2	US0264	DNA mismatch endon
868	33	68.8	543	2	S35047	glucubin-1S, huma	941	32	66.7	157	2	F95313	hypothetical prote
869	33	68.8	573	2	A53234	glucubin-1S, huma	942	32	66.7	161	2	H85120	probable prolins-r
870	33	68.8	574	2	T04249	hypothetical prote	943	32	66.7	162	2	A55969	F2P1 protein - si
871	33	68.8	582	2	B53234	vicilin-like stora	944	32	66.7	163	2	D87293	Fur family protein
872	33	68.8	583	2	T12576	probable phosphate	945	32	66.7	164	2	T07759	disease resistance
873	33	68.8	609	2	F84824	hypothetical prote	946	32	66.7	168	2	T22447	hypothetical prote
874	33	68.8	610	2	S35049	mucin JER57 - huma	947	32	66.7	171	2	T10904	sportamin - sweet
875	33	68.8	615	2	T20839	hypothetical prote	948	32	66.7	171	2	A83458	urase accessory p
876	33	68.8	638	2	T47569	hypothetical prote	949	32	66.7	172	2	T00924	hypothetical prote
877	33	68.8	647	2	C96834	unknown protein P5	950	32	66.7	172	2	D82642	conserved hypotnet
878	33	68.8	647	2	T26240	hypothetical prote	951	32	66.7	173	2	B41841	hypothetical prote
879	33	68.8	695	2	C86731	copper-potassum t	952	32	66.7	173	2	A18172	bilin biosynthesis
880	33	68.8	697	2	B86239	protein T10024.19	953	32	66.7	174	2	B69979	urase accessory p
881	33	68.8	702	2	T27730	hypothetical prote	954	32	66.7	185	2	G64075	urase accessory p
882	33	68.8	720	2	J01676	AB13 protein - Ara	955	32	66.7	185	2	T51844	RING-H2 finger pro
883	33	68.8	754	2	S50601	hypothetical prote	956	32	66.7	190	1	WMBE28	structural phospho
884	33	68.8	764	2	T48446	hypothetical prote	957	32	66.7	195	2	AC0778	probable membrane
885	33	68.8	800	2	S54623	probable mitochon	958	32	66.7	195	2	T21300	hypothetical prote
886	33	68.8	833	2	T01547	probable phosphol	959	32	66.7	195	2	AD0024	peptidylprolyl iso
887	33	68.8	839	2	B96576	hypothetical prote	960	32	66.7	203	2	G85850	hypothetical prote
888	33	68.8	853	2	S74279	hypothetical prote	961	32	66.7	203	2	F64981	hypothetical 22.4
889	33	68.8	1042	2	T25644	hypothetical prote	962	32	66.7	203	2	F91006	hypothetical prote
890	33	68.8	1440	2	T33813	hypothetical prote	963	32	66.7	204	2	G83482	probable transcrip
891	33	68.8	1476	2	A45773	kelch protein, lon	964	32	66.7	205	2	F85363	hypothetical prote
892	33	68.8	2145	2	JC4747	adenylate cyclase	965	32	66.7	211	2	C84751	hypothetical prote
893	33	67.7	2145	2	B96750	hypothetical prote	966	32	66.7	213	2	C84200	hypothetical prote
894	33.5	67.7	512	2	T23166	hypothetical prote	967	32	66.7	219	2	T05653	proline-rich phosp
895	32	66.7	13	2	AB0764	his operon leader	968	32	66.7	225	2	C88633	protein P5683.3 (i
896	32	66.7	69	2	S17518	opa protein - fru1	969	32	66.7	230	2	T19161	dyctonin isoform 2
897	32	66.7	69	2	AE2474	hypothetical prote	970	32	66.7	232	2	T16873	hypothetical prote
898	32	66.7	73	2	T18013	hypothetical prote	971	32	66.7	234	2	T34301	hypothetical prote
899	32	66.7	83	2	A44465	sodium ion pump ox	972	32	66.7	236	2	C82566	hypothetical prote
900	32	66.7	87	2	T16439	hypothetical prote	973	32	66.7	241	2	H84864	hypothetical prote
901	32	66.7	88	2	AP1283	conserved hypotnet	974	32	66.7	243	2	T51652	myb-related transc
902	32	66.7	88	2	A11654	conserved hypotnet	975	32	66.7	244	2	T00449	hypothetical prote
903	32	66.7	94	2	S32939	Au1 protein - yea	976	32	66.7	244	2	H84853	hypothetical prote
904	32	66.7	97	2	T23850	hypothetical prote	977	32	66.7	244	2	JC2379	cell-specific heli
905	32	66.7	102	2	AD1420	PTS cellobiose-spe	978	32	66.7	245	2	S10658	hypothetical prote

```

979 32 66.7 245 2 G72064 ABC transporter AT
980 32 66.7 245 2 B86558 ABC transporter AT
981 32 66.7 248 2 S20866 MADS box protein s
982 32 66.7 250 2 T36868 hypothetical prote
983 32 66.7 251 2 AG0132 probable hydroxyc
984 32 66.7 257 2 AC1879 hypothetical prote
985 32 66.7 257 2 S01165 acetate-acute locu
986 32 66.7 260 2 T18909 hypothetical prote
987 32 66.7 264 2 PNO681 nitrogenase (EC 1.
988 32 66.7 271 2 T49956 myb-related protei
989 32 66.7 273 1 S69189 myb-related protei
990 32 66.7 276 2 AH0244 probable esterase
991 32 66.7 276 2 T51685 myb-related transc
992 32 66.7 278 1 S57643 stearyl-CoA 9-des
993 32 66.7 278 2 H64029 hypothetical prote
994 32 66.7 278 2 T49276 hypothetical prote
995 32 66.7 279 2 B66402 protein T22C5.19 [
996 32 66.7 281 2 E64216 hypothetical prote
997 32 66.7 285 2 T05777 hypothetical prote
998 32 66.7 288 2 G06629 Rev interacting pr
999 32 66.7 289 2 T01257 probable GT-1-like
1000 32 66.7 290 2 T36205 hypothetical prote

```

ALIGNMENTS

```

RESULT 1
LFECH
his operon leader peptide - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004
C:Accession: A03594; I41073; A64967
R:Verde, P.; Funzio, R.; di Nocera, P. P.; Blasi, F.; Bruni, C.B.
Nucleic Acids Res. 9, 2075-2086, 1981
A:Title: Identification, nucleotide sequence and expression of the regulatory region of
A:Reference number: A03594; MUID:82059525; PMID:6170941
A:Accession: A03594
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: UNIPROT:P60995; UNIPARC:UPI000012E854; GB:V00284; GB:J01627; GB:J016
A>Note: this protein is involved in the attenuation mechanism for the control of the exp
R:Di Nocera, P. P.; Blasi, F.; Di Lauro, R.; Funzio, R.; Bruni, C.B.
Proc. Natl. Acad. Sci. U.S.A. 75, 4276-4280, 1978
A:Title: Nucleotide sequence of the attenuator region of the histidine operon of Escheri
A:Reference number: I41073; MUID:79033821; PMID:360215
A:Accession: I41073
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: UNIPARC:UPI000012E854; EMBL:V00285; NID:G41701; PIDN:CAA23550.1; PID
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A64967
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-16 <BLAT>
A:Cross-references: UNIPARC:UPI000012E854; GB:AE000293; GB:U00096; NID:G2367127; PIDN:AE
A:Experimental source: strain K-12, substrain W61655
C:Genetics:
A:Gene: hisl
A:Superfamily: his leader peptide
C:Keywords: histidine biosynthesis

```

```

Db 8 HHHHHH 13
RESULT 2
his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain RMD
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: C90981
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A96629; MUID:21156231; PMID:11258796
A:Accession: C90981
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <RAY>
A:Cross-references: UNIPROT:Q8X8T5; UNIPARC:UPI0000D08D2; GB:BA000007; PIDN:BA036242.1,
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC82819

```

```

Query Match 100.0%; Score 48; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 HHHHHH 6
Db 9 HHHHHH 14

```

```

RESULT 3
his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85827
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85827
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-16 <STO>
A:Cross-references: UNIPROT:Q8X8T5; UNIPARC:UPI0000D08D2; GB:AE005174; NID:G12516199; P
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: hisl

```

```

Query Match 100.0%; Score 48; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 HHHHHH 6
Db 9 HHHHHH 14

```

```

RESULT 4
hisidine and glutamine-rich protein - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: H64698
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodex, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpik, P.D.; Smith, H.O.; Fraser, C
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

```

A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: H64698
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-57 <TOM>
 A:Cross-references: UNIPROT:O25973; UNIPARC:UPI000017A919; GB:AE000511; TIGR:HP1432

Query Match
 Best Local Similarity 100.0%; Score 48; DB 2; Length 57;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 16 HHHHHH 21

RESULT 5
 C64698
 Probable histidine-rich metal-binding protein - Helicobacter pylori
 C:Species: Helicobacter pylori
 A:Variety: strain J99, 26695
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: C64698; C71821
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalik, H.G.; Glodex, A.; McKenna, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frazer, C.
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: C64698
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-60 <TOM>
 A:Cross-references: UNIPROT:Q48251; UNIPARC:UPI000014897A; GB:AE000643; GB:AE000511; NID:16436
 A:Experimental source: strain 26695
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: C71821
 A:Molecule type: DNA
 A:Residues: 1-60 <ARN>
 A:Cross-references: UNIPARC:UPI000014897A; GB:AE001555; GB:AE001439; NID:G4155929; PIDN: A:Experimental source: strain J99
 C:Genetics:
 A:Gene: HP1427; jhp1320

Query Match
 Best Local Similarity 100.0%; Score 48; DB 2; Length 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 11 HHHHHH 16

RESULT 6
 S57787
 Hypothetical protein 2 (clone EST) - barley
 C:Species: Hordeum vulgare (barley)
 C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S57787
 R:Spelman, E.; Salamini, F.; Plant Mol. Biol. 28, 915-926, 1995
 A:Title: GA(3)-regulated cDNAs from Hordeum vulgare leaves.
 A:Reference number: S57787; MUID:95367651; PMID:7640362
 A:Accession: S57787
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-64 <SP>
 A:Cross-references: UNIPROT:Q40049; UNIPARC:UPI000009D67D; EMBL:X78884; NID:G929666; PID

Query Match
 Best Local Similarity 100.0%; Score 48; DB 2; Length 64;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 25 HHHHHH 30

RESULT 7
 D71821
 Probable histidine and glutamine-rich metal-binding protein - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: D71821
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: D71821
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 <ARN>
 A:Cross-references: UNIPROT:Q92J18; UNIPARC:UPI00000D3729; GB:AE001555; GB:AE001439; NID: A:Experimental source: strain J99
 C:Genetics:
 A:Gene: jhp1321

Query Match
 Best Local Similarity 100.0%; Score 48; DB 2; Length 77;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 21 HHHHHH 26

RESULT 8
 T16436
 Hypothetical protein F53A9.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T16436
 R:Miller, N.
 A:Description: The sequence of C. elegans cosmid F53A9.
 A:Reference number: Z18513
 A:Accession: T16436
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-77 <ML>
 A:Cross-references: UNIPROT:Q20690; UNIPARC:UPI000007C69D; EMBL:U23523; NID:G746551; PI: A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:F53A9.1

Query Match
 Best Local Similarity 100.0%; Score 48; DB 2; Length 77;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 46 HHHHHH 51

RESULT 9
 T16435
 Hypothetical protein F53A9.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

```

C/Accession: T16435
R/Miller, N.
submitted to the EMBL Data Library, March 1995
A/Description: The sequence of C. elegans cosmid F53A9.
A/Reference number: Z18513
A/Accession: T16435
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-83 <ML>
A/Cross-references: UNIPROT:Q20689; UNIPARC:UPI000007808B; EMBL:U23523; NID:g746551; PID
A/Experimental source: strain Bristol N2
C/Genetics:
A/Gene: CESP:F53A9.2

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 45 HHHHHH 50

RESULT 10
T34146
hypothetical protein C33H5.13 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
A/Accession: T34146
R/Bradshaw, H.; Stellyes, L.
submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid C33H5.
A/Reference number: Z21482
A/Accession: T34146
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-92 <BR>
A/Cross-references: UNIPROT:Q18410; UNIPARC:UPI0000079A72; EMBL:U41007; PIDN:AAA82273.1;
A/Experimental source: strain Bristol N2
C/Genetics:
A/Gene: CESP:C33H5.13
A/Introns: 13/3; 53/2

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 58 HHHHHH 63

RESULT 11
B4971
hypothetical protein 2 - Plasmodium brasiliannum
C/Species: Plasmodium brasiliannum
C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
A/Accession: B4971
R/Kilejian, A.; Yang, Y.F.; Cochran, A.H.; Rashid, M.A.
Mol. Biochem. Parasitol. 38, 291-295, 1990
A/Title: Homologous sequences in Plasmodium cynomolgi and the gene of the histidine-rich
A/Reference number: A44971; MUID:90220761; PMID:2183051
A/Accession: B44971
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-101 <KIT>
A/Cross-references: UNIPROT:Q25652; UNIPARC:UPI000017B5D; GB:M28064

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 101;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6

```

```

Db 5 HHHHHH 10

RESULT 12
T30119
hypothetical protein F22H10.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A/Accession: T30119
R/Langston, Y.; Hawkins, J.
submitted to the EMBL Data Library, September 1996
A/Description: The sequence of C. elegans cosmid F22H10.
A/Reference number: Z20740
A/Accession: T30119
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-102 <LAN>
A/Cross-references: UNIPROT:Q94189; UNIPARC:UPI000007E413; EMBL:U70845; PIDN:AAB09100.1;
A/Experimental source: strain Bristol N2; clone F22H10
C/Genetics:
A/Gene: CESP:F22H10.2
A/Map position: X
A/Introns: 16/1

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 102;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 61 HHHHHH 66

RESULT 13
S37150
aer2 protein - tomato
C/Species: Lycopersicon esculentum (tomato)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
A/Accession: S37150
R/Amitai, H.; Scolnik, P.A.; Bar-Zvi, D.
submitted to the EMBL Data Library, September 1993
A/Reference number: S37150
A/Accession: S37150
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <AMT>
A/Cross-references: UNIPROT:P37219; UNIPARC:UPI0000126164; EMBL:X74907; NID:g400468; PID
C/Genetics:
A/Introns: 53/3

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 114;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 108 HHHHHH 113

RESULT 14
H72583
hypothetical protein APE1948 - Aeropyrum pernix
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
A/Accession: H72583
R/Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatake, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: H72583
A/Status: preliminary

```

A:Molecule type: DNA
A:Residues: 1-115 <KAM>
A:Cross-references: UNIPROT:O9YAJ2; UNIPARC:UPI000005E159; DDBJ:AF000062; NID:G5105244;
A:Experimental source: strain KI
C:Genetics:
A:Gene: APE1948

Query Match 100.0%; Score 48; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.99; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
Db 32 HHHHHH 37

RESULT 15

T01558
auxin-induced protein homolog A.TW018A10.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 31-Dec-2004
C:Accession: T01558
R:Dempsey, S.; Harper, M.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of A. thaliana TW018A10.
A:Reference number: Z14348
A:Accession: T01558
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-122 <DEM>
A:Cross-references: UNIPROT:O23089; UNIPARC:UPI000004A87A; EMBL:AF013294; NID:G2252848;
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Note: A.TW018A10.6
C:Superfamily: auxin-induced protein 10A

Query Match 100.0%; Score 48; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
Db 108 HHHHHH 113

RESULT 16

S14983
extensin class I (clone w10-1 L) - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C>Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 17-Jul-1998
C:Accession: S14983
R>Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A>Title: Tomato extensin and extensin-like CDNA: structure and expression in response to
A:Reference number: S14970; MUID:91329690; PMID:1714316
A:Accession: S14983
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <SHO>
A:Cross-references: UNIPARC:UPI000017B08A; EMBL:X55694
A:Experimental source: cv. UC82B
C:Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
Db 54 HHHHHH 59

RESULT 17

I39193
gene HOXA1 protein - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
C:Accession: I39193
R:Charlot, A.; Moreau, L.; Senterre, G.; Sobel, M.; Castronovo, V.
Biochem. Biophys. Res. Commun. 215, 713-720, 1995
A>Title: Retinoic acid induces three newly cloned HOXA1 transcripts in MCF7 breast cancer
A:Reference number: I39192; MUID:96011836; PMID:7488013
A:Accession: I39193
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-132 <RES>
A:Cross-references: UNIPARC:UPI000015FF40; EMBL:U73431; NID:G1051226; PIDN:AAC50250.1; P
C:Genetics:
A:Gene: GDB:HOXA1
A:Cross-references: GDB:120652; OMIM:142955
A:Map position: 7p15.3-7p15.3
A:Introns: 113/3
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 100.0%; Score 48; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
Db 60 HHHHHH 65

RESULT 18

B30242
stem cell protein ERA-1-199, retinoic acid-induced - mouse
C:Species: Mus musculus (house mouse)
C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Dec-2004
C:Accession: B30242
R:LaRosa, G.J.; Gudas, L.J.
Mol. Cell. Biol. 8, 3906-3917, 1988
A>Title: Early retinoic acid-induced f9 teratocarcinoma stem cell gene ERA-1: alternate
A:Reference number: A30242; MUID:89127233; PMID:2906112
A:Accession: B30242
A:Molecule type: mRNA
A:Residues: 1-133 <LAR>
A:Cross-references: UNIPROT:P09022; UNIPARC:UPI000002AB6D; GB:M22115; NID:G193047; PIDN:
C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulation

Query Match 100.0%; Score 48; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
Db 60 HHHHHH 65

RESULT 19

T22959
hypothetical protein F58H10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22959
R:McMurray, A.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z19643
A:Accession: T22959
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-136 <MII>
A:Cross-references: UNIPROT:O93827; UNIPARC:UPI000007ERCA; EMBL:Z79697; PIDN:CAB01975.1;
A:Experimental source: clone F58H10
C:Genetics:
A:Gene: CESP:F58H10.1

A:Map position: 1
A:introns: 103/2

Query Match 100.0%; Score 48; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 HHHHHH 6
|||||
DB 77 HHHHHH 82

RESULT 20
T33968
hypothetical protein F46E10.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33968
R:Johnson, D.; Bradshaw, H.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid F46E10.
A:Reference number: Z21446
A:Accession: T33968
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-139 <JH>
A:Cross-references: UNIPROT:Q9UAV7; UNIPARC:UPI000007704D; EMBL:AF125955; P1DN:ADU14713.
C:Genetic8:
A:Gene: CESP:F46E10.2
A:Map position: 5
A:introns: 22/1; 82/2

Query Match 100.0%; Score 48; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 HHHHHH 6
|||||
DB 121 HHHHHH 126

RESULT 21
T06554
probable profilin PRO3 - wheat
C:Species: *Triticum aestivum* (common wheat)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06554
R:Rihns, H.P.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z15756
A:Accession: T06554
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-140 <RIH>
A:Cross-references: UNIPROT:P49234; UNIPARC:UPI0000132294; EMBL:X89827; NID:G1008444; PI
A:Experimental source: cv. Tam 107; 13 day seedlings
C:Genetics:
A:Gene: PRO3
C:Superfamily: profilin
C:Keywords: actin binding; cytoskeleton

Query Match 100.0%; Score 48; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 HHHHHH 6
|||||
DB 135 HHHHHH 140

RESULT 22
A54523

histidine-rich protein - *Plasmodium lophurae* (fragment)
C:Species: *Plasmodium lophurae*
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 31-Dec-2004
C:Accession: A54523
R:Irving, D.O.; Cross, G.A.M.; Feder, R.; Wallach, M.
Mol. Biochem. Parasitol. 18, 223-234, 1986
A>Title: Structure and organization of the histidine-rich protein gene of *Plasmodium lopi*
A:Reference number: A54523; MUID:86174893; PMID:3007981
A:Accession: A54523
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <IRV>
A:Cross-references: UNIPROT:Q26056; UNIPARC:UPI000007C1E6; GB:M15317; NID:G160331; P1DN:
C:Superfamily: surface antigen spar
C:Keywords: tandem repeat

Query Match 100.0%; Score 48; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 HHHHHH 6
|||||
DB 1 HHHHHH 6

RESULT 23
T19083
hypothetical protein C08B6.10 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19083
R:Wilkinson, J.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19070
A:Accession: T19083
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-140 <WIL>
A:Cross-references: UNIPROT:Q17821; UNIPARC:UPI00000793A5; EMBL:Z72502; P1DN:CAA96592.1;
A:Experimental source: clone C08B6
C:Genetics:
A:Gene: CESP:C08B6.10
A:Map position: 5
A:introns: 22/2

Query Match 100.0%; Score 48; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 HHHHHH 6
|||||
DB 102 HHHHHH 107

RESULT 24
T06553
probable profilin PRO2 - wheat
C:Species: *Triticum aestivum* (common wheat)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06553
R:Rihns, H.P.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z15756
A:Accession: T06553
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-141 <RIH>
A:Cross-references: UNIPROT:P49233; UNIPARC:UPI000013228A; EMBL:X89826; NID:G1008442; PI
A:Experimental source: cv. Tam 107; 13 day seedlings
C:Genetics:
A:Gene: PRO2
C:Superfamily: profilin
C:Keywords: actin binding; cytoskeleton

Query Match 100.0%; Score 48; DB 2; length 141;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 136 HHHHHH 141

RESULT 25

B64421 conserved hypotheoretical protein MJ0970 - Methanococcus jannaschii

C/Species: Methanococcus jannaschii
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Jul-2004

C/Accession: B64421
 R/Bult, C.U.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 ; Reich, C.I.; Overbeek, R.; Kikness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodok, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996

A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
 A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A/Reference number: A64300; MUID:9633799; PMID:8688087

A/Accession: B64421

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-143 <BU>

A/Cross-references: UNIPROT:O58380; UNIPARC:UPI000013959A; GB:U67540; GB:L77117; NID:915

C/Genetics:

A/Map position: REV904629-904198

C/Superfamily: cobaltochelatase/ferrochelatase CblX/SirB

Query Match 100.0%; Score 48; DB 1; length 143;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 99 HHHHHH 104

RESULT 26

T51065

hypotheoretical protein B12F1.170 [imported] - Neurospora crassa

C/Species: Neurospora crassa

C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000

C/Accession: T51065

R/Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, July 2000

A/Reference number: Z25266

A/Accession: T51065

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-172 <SCH>

A/Cross-references: UNIPARC:UPI0000179F4B; EMBL:AL390091; GSPDB:GN00116; NCSP:B12F1.170

A/Experimental source: BAC clone B12F1; strain OR74A

C/Genetics:

A/Gene: NCSP:B12F1.170

A/Map position: 6

A/Introns: 51/3; 125/2

C/Superfamily: Neurospora crassa hypotheoretical protein B12F1.170

Query Match 100.0%; Score 48; DB 2; length 172;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 83 HHHHHH 88

RESULT 27

T48265

hypotheoretical protein T22P11.30 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C/Accession: T48265

R/Beyan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, April 2000

A/Reference number: Z24490

A/Accession: T48265

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-176 <BY>

A/Cross-references: UNIPROT:O9LZ58; UNIPARC:UPI00009DABC; EMBL:AL162971

A/Experimental source: cultivar Columbia; BAC clone T22P11

C/Genetics:

A/Map position: 5

A/Introns: 4/3; 61/3

A/Note: T22P11.30

Query Match 100.0%; Score 48; DB 2; length 176;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 27 HHHHHH 32

RESULT 28

B64774

probable RING zinc finger protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: B64774

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Wolfat, K.S.; Cronin, L.A.; Shen, M.; Yankem, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A64420; MUID:20083487; PMID:10617197

A/Accession: B64774

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-180 <STO>

A/Cross-references: UNIPROT:O9SJS9; UNIPARC:UPI000009EB11; GB:AE002093; NID:94510378; P

C/Genetics:

A/Gene: At2g35910

A/Map position: 2

Query Match 100.0%; Score 48; DB 2; length 180;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 71 HHHHHH 76

RESULT 29

T39367

hypotheoretical protein SPBC1289.16c - fission yeast (Schizosaccharomyces pombe) (fragment)

C/Species: Schizosaccharomyces pombe

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T39367

R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.

submitted to the EMBL Data Library, March 1999

A/Reference number: Z21848

A/Accession: T39367

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-192 <WOO>

A/Cross-references: UNIPROT:O42890; UNIPARC:UPI0000162111; EMBL:AL035675; PIDN:CAB3869

A/Experimental source: strain 972h-; cosmid c1289

C/Genetics:

A:Gene: SPDB:SPBC1289.16c
A:Map position: 2

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 192;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
Db 140 HHHHHH 145

RESULT 30

T25384
hypochemical protein T27F6.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25384

R:DoBson, R.
submitted to the EMBL Data Library, November 1996
A:Accession: T25384
A:Reference number: 220026

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-206 <WII>
A:Cross-references: UNIPROT:O45868; UNIPARC:UPI000007F4F2; EMBL:Z82060; PIDN:CAB04883.1;
A:Experimental source: clone T27F6
C:Genetics:

A:Gene: CESP:T27F6.4
A:Map position: 1
A:Introns: 61/3; 154/3

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 206;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
Db 116 HHHHHH 121

RESULT 31

T24446
hypochemical protein T04C10.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24446

R:Burton, J.
submitted to the EMBL Data Library, March 1996
A:Reference number: 219891
A:Accession: T24446

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-208 <WII>
A:Cross-references: UNIPROT:Q22156; UNIPARC:UPI000007C102; EMBL:Z69885; PIDN:CAA93757.1;
A:Experimental source: clone T04C10
C:Genetics:

A:Gene: CESP:T04C10.4
A:Map position: X
A:Introns: 91/3; 183/3

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 208;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
Db 30 HHHHHH 35

RESULT 32

I53100
eHAND - mouse

C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I53100

R:Caerjeff, P.; Brown, D.; Lyons, G.E.; Olson, E.N.
Dev. Biol. 170, 664-678, 1995
A:Title: Expression of the novel basic helix-loop-helix gene eHAND in neural crest deriv

A:Reference number: I53100; MUID:95377552; PMID:7649392
A:Accession: I53100

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-216 <RES>
A:Cross-references: UNIPARC:UPI0000024164; GB:S79216; NID:g1086931; PIDN:AAB35104.1; PII

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 216;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
Db 9 HHHHHH 14

RESULT 33

T32443
hypochemical protein T28B4.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T32443

R:Wilson, R.; Greco, T.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T28B4.
A:Reference number: 221168

A:Accession: T32443
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-219 <WII>
A:Cross-references: UNIPARC:UPI000017BBFB; EMBL:AF026206; PIDN:AAB71260.1; GSPDB:GN00028

A:Experimental source: strain Bristol N2; clone T28B4
C:Genetics:
A:Gene: CESP:T28B4.4
A:Map position: X
A:Introns: 34/2; 138/2; 184/3

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 219;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
Db 38 HHHHHH 43

RESULT 34

I59192
gene HOXA1 protein - human

C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
C:Accession: I59192

R:Charlot, A.; Moreau, L.; Senterre, G.; Sobel, M.; Castronovo, V.
Biochem. Biophys. Res. Commun. 215, 713-720, 1995
A:Title: Retinoic acid induces three newly cloned HOXA1 transcripts in MCF7 breast cancer

A:Reference number: I59192; MUID:96011836; PMID:7488013
A:Accession: I59192

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-222 <RES>

A:Cross-references: UNIPARC:UPI000016A264; EMBL:U37431; NID:g1051226; PIDN:AAC50248.1; P
C:Genetics:
A:Gene: GDB:HOXA1
A:Cross-references: GDB:120652; OMIM:142955
A:Map position: 7p15.3-7p15.3

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

```

Query Match          100.0%; Score 48; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
    |||||
Db 60 HHHHHH 65

RESULT 35
T47866
regulatory protein-like - Arabidopsis thaliana
N:Alternate names: protein T8B10.210
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 12-Jul-2004
C:Accession: T47866
R:Reiger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224478
A:Accession: T47866
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <RIB>
A:CROSS-references: UNIPROT:Q9M205; UNIPARC:UPI000009F73B; EMBL:AL138646
C:Genetics:
A:Map position: 3
A:introns: 137/2
A>Note: T8B10.210
C:Superfamily: negative regulatory factor PRG

Query Match          100.0%; Score 48; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
    |||||
Db 218 HHHHHH 223

RESULT 36
D89101
protein F25E5.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89101
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: See websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elg
A>Note: published extra appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D89101
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-235 <STO>
A:CROSS-references: UNIPROT:Q76647; UNIPARC:UPI000007715A; GB:chr_V; PIRN:AA027331.1; PI
A:Genetics:
A>Note: weak similarity to POU transcription factors
A:Gene: F25E5.8
A:Map position: 5

Query Match          100.0%; Score 48; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
    |||||
Db 114 HHHHHH 119

RESULT 37
S41512

```

```

Brn-3b protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Dec-1994 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
C:Accession: S41512
R:Theil, T.; McLean-Hunter, S.; Zoernig, M.; Moeroy, T.
Nucleic Acids Res. 21, 5921-5929, 1993
A>Title: Mouse Brn-3 family of POU transcription factors: a new aminoterminal domain is
A:Reference number: S41511; MUID:94119691; PMID:8290353
A:Accession: S41512
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-236 <THE>
A:CROSS-references: UNIPARC:UPI0000E5952
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:91-161/Domain: POU domain homology <POU>
F:180-236/Domain: homeobox homology <HOX>

Query Match          100.0%; Score 48; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
    |||||
Db 78 HHHHHH 83

RESULT 38
E86346
F16F4.1 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86346
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:1130712
A:Accession: E86346
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-239 <STO>
A:CROSS-references: UNIPROT:Q9LMP5; UNIPARC:UPI0000A94EA; GB:AE005172; NID:G8920630; P
A:Genetics:
A:Map position: 1

Query Match          100.0%; Score 48; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
    |||||
Db 154 HHHHHH 159

RESULT 39
S41511
Brn-3a protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Dec-1994 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
C:Accession: S41511
R:Theil, T.; McLean-Hunter, S.; Zoernig, M.; Moeroy, T.
Nucleic Acids Res. 21, 5921-5929, 1993
A>Title: Mouse Brn-3 family of POU transcription factors: a new aminoterminal domain is
A:Reference number: S41511; MUID:94119691; PMID:8290353
A:Accession: S41511
A:Status: preliminary
A:Molecule type: mRNA

```

A;Residues: 1-255 <THE>
 A;Cross-references: UNIPARC:UPI000017A2E0
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;110-180/Domain: POU domain homology <POU>
 F;199-255/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 48; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 100 HHHHHH 105

RESULT 40
 T51679
 myb-related transcription factor MYB74 [imported] - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 31-Dec-2004
 C;Accession: T51679
 R;Kranz, H.D.; Denekamp, M.; Greco, R.; Yin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J
 Paz-Ares, J.; Weisbecker, B.
 Plant J. 16, 263-276, 1998
 A;Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
 A;Reference number: 214349; MUID:9839469; PMID:9839469
 A;Accession: T51679
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
 A;Residues: 1-259 <KRA>
 A;Cross-references: UNIPROT:Q9ZTC8; UNIPARC:UPI00009052B; EMBL:AF062907; PIDN:MAC83629.
 A;Experimental source: cultivar Columbia
 C;Genetics:
 A;Gene: MYB74
 A;Map position: IV
 C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
 C;Keywords: transcription factor

Query Match 100.0%; Score 48; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 84 HHHHHH 89

RESULT 41
 A70359
 hydrogenase expression/formation protein B - Aquifex aeolicus
 C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 31-Dec-2004
 C;Accession: A70359
 R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
 V.
 Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; MUID:98196666; PMID:9537320
 A;Accession: A70359
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-259 <AOE>
 A;Cross-references: UNIPROT:O66901; UNIPARC:UPI0000563FF; GB:AE000701; NID:g2983260; PI
 C;Experimental source: strain VFS
 C;Genetics:
 A;Gene: hupB
 C;Superfamily: N1(2+)-binding GTPase ([N1fe]-hydrogenase/urease maturation factor)

Query Match 100.0%; Score 48; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6

DB 18 HHHHHH 23

RESULT 42
 B66300
 protein F309.30 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: B66300
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federopiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.,
 ansen, N.F.; Hughes, B.; Huizart, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltli, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A66141; MUID:21016719; PMID:11130712
 A;Accession: B66300
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-259 <STO>
 A;Cross-references: UNIPROT:Q9SA48; UNIPARC:UPI00005EB54; GB:AE005172; NID:g4966370; PI
 C;Genetics:
 A;Map position: 1
 C;Superfamily: Arabidopsis thaliana hypothetical protein YUPH12R.23

Query Match 100.0%; Score 48; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 96 HHHHHH 101

RESULT 43
 A56446
 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
 C;Species: Mus musculus (house mouse)
 C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
 C;Accession: A56446
 R;Tang, P.M.; Folter, L.A.; Mahoney, W.C.; Schueler, P.A.
 J. Biol. Chem. 270, 7829-7835, 1995
 A;Title: A high affinity disoxin-binding protein displayed on M13 is functionally identifi
 A;Reference number: A56446; MUID:95229583; PMID:7713873
 A;Accession: A56446
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-268 <TAN>
 A;Cross-references: UNIPARC:UPI000017C6D0; GB:U20617
 C;Keywords: heterodimer; immunoglobulin

Query Match 100.0%; Score 48; DB 2; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 246 HHHHHH 251

RESULT 44
 F96506
 hypothetical protein T12C22.4 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: F96506
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federopiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.,

ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lures, J.S.; Maici, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A66141; MUID:21016719; PMID:11130712
 A:Accession: P96506
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-269 <STO>
 A:Cross-references: UNIPROT:Q9LPR4; UNIPARC:UPI00000A76A7; GB:AE005173; NID:g8655987; PI
 A:Genetics:
 A:Gene: T12C22.4
 A:Map position: 1

Query Match 100.0%; Score 48; DB 2; Length 269;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
 |||||
 Db 28 HHHHHH 33

RESULT 45
 A26480
 knob protein - malaria parasite (*Plasmodium falciparum*) (fragments)
 C:Species: *Plasmodium falciparum*
 C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
 C:Accession: A26480
 R:Kilejian, A.; Sharma, Y.D.; Karoui, H.; Naslund, L.
 Proc. Natl. Acad. Sci. U.S.A. 83, 7938-7941, 1986
 A:Title: Histidine-rich domain of the knob protein of the human malaria parasite *Plasmod*
 A:Reference number: A26480; MUID:87017062; PMID:3532126
 A:Accession: A26480
 A:Molecule type: mRNA
 A:Residues: 1-270 <KIL>
 A:Cross-references: UNIPROT:P09346; UNIPARC:UPI000016BP96; GB:M14210; NID:g160361; PIDN:
 C:Superfamily: knob-associated histidine-rich protein

Query Match 100.0%; Score 48; DB 2; Length 270;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
 |||||
 Db 63 HHHHHH 68

RESULT 46
 T02334
 probable urease accessory protein [imported] - *Arabidopsis thaliana*
 N:Alternate names: urease accessory protein G homolog F13P17.30
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 31-Dec-2004
 C:Accession: T02334; A84757
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, July 1998
 A:Description: *Arabidopsis thaliana* chromosome II BAC F13P17 genomic sequence.
 A:Reference number: 214657
 A:Accession: T02334
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-275 <ROU>
 A:Cross-references: UNIPROT:O64700; UNIPARC:UPI000000C5C0; EMBL:AC004481; NID:g3337347;
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Mofat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
 eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J
 Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84757
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <STO>
 A:Cross-references: UNIPARC:UPI000000C5C0; GB:AE002093; NID:g3128220; PIDN:AAC26700.1; G
 A:Genetics:
 A:Gene: At2g34470; F13P17.30
 A:Map position: 2
 A:introns: 18/2; 85/2; 105/3; 173/1; 213/3; 248/3
 C:Superfamily: N1(2+)-binding GTPase ([N1fe]-hydrogenase/urease maturation factor)

Query Match 100.0%; Score 48; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
 |||||
 Db 6 HHHHHH 11

RESULT 47
 E84766
 probable AT-hook DNA-binding protein [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 05-Oct-2004
 C:Accession: E84766
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Mofat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
 eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84766
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-285 <STO>
 A:Cross-references: UNIPROT:O82166; UNIPARC:UPI00000A14DC; GB:AE002093; NID:g3668079; PI
 C:Genetics:
 A:Gene: At2g35270
 A:Map position: 2
 C:Superfamily: AT-hook DNA-binding protein

Query Match 100.0%; Score 48; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
 |||||
 Db 40 HHHHHH 45

RESULT 48
 T21868
 hypothetical protein F36G9.11 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T21868
 R:Wall, M.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: 219481
 A:Accession: T21868
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-290 <WIL>
 A:Cross-references: UNIPROT:O45469; UNIPARC:UPI0000061011; EMBL:Z81533; PIDN:CAB04330.1
 A:Experimental source: clone F36G9
 C:Genetics:
 A:Gene: CESP:F36G9.11
 A:Map position: 5
 A:introns: 130/3; 234/2

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:00:40 ; Search time 235 Seconds
(without alignments)
18.013 Million cell updates/sec

Title: US-10-719-523-5
Perfect score: 48
Sequence: 1 HHHHHH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	15	1 LPHI_YERPE	Q8d079 yerxina pe
2	48	100.0	16	1 LPHI_ECO57	Q8x8t5 escherichia
3	48	100.0	16	1 LPHI_ECOL6	P60996 escherichia
4	48	100.0	16	1 LPHI_ECOL1	P60995 escherichia
5	48	100.0	16	1 LPHI_KUEPN	Q48439 klebsiella
6	48	100.0	16	1 LPHI_SALT9	P60997 salmonella
7	48	100.0	30	2 Q5C5K5_SCHJA	Q5C5K5 schistosoma
8	48	100.0	31	2 Q6UGP2_PEA	Q6UGP2 pium sativ
9	48	100.0	31	2 Q6UGP3_PEA	Q6UGP3 pium sativ
10	48	100.0	31	2 Q6UGP5_PEA	Q6UGP5 pium sativ
11	48	100.0	31	2 Q6UGP7_PEA	Q6UGP7 pium sativ
12	48	100.0	31	2 Q5S0G0_MOUSE	Q5S0G0 mus musculu
13	48	100.0	34	2 Q4YAH2_PLABE	Q4YAH2 plasmodium
14	48	100.0	44	2 Q658Z5_PBAKU	Q658Z5 unidentified
15	48	100.0	46	2 Q5ISM1_MACFA	Q5ISM1 macaca fasc
16	48	100.0	48	2 Q8SAS0_PINSY	Q8SAS0 pinus sylve
17	48	100.0	48	2 Q8SAS1_PINSY	Q8SAS1 pinus sylve
18	48	100.0	53	2 Q5C2J2_SCHJA	Q5C2J2 schistosoma
19	48	100.0	53	2 Q55244_92ZZZ	Q55244 plasmod pet
20	48	100.0	54	2 Q4WHB8_ASPFU	Q4WHB8 aspergillus
21	48	100.0	58	2 Q6THI9_DROME	Q6THI9 drosophila
22	48	100.0	59	1 HEN_HELPU	P0A8V7 helicobacte
23	48	100.0	59	1 HEN_HELPU	P0A8V6 helicobacte
24	48	100.0	64	2 Q40049_HORVU	Q40049 hordeum vul
25	48	100.0	66	2 Q6IJH9_DROME	Q6IJH9 drosophila
26	48	100.0	69	2 Q6R2V8_TRIRE	Q6R2V8 trichoderma
27	48	100.0	69	2 Q4TOL0_GIBZE	Q4TOL0 gibberella
28	48	100.0	69	2 Q9PT65_XENTL	Q9PT65 xenopus lae
29	48	100.0	72	2 Q54KT2_DICDI	Q54KT2 dictyostei
30	48	100.0	72	2 Q8T1A1_DICDI	Q8T1A1 dictyostei
31	48	100.0	72	2 Q25973_HELPU	Q25973 helicobacte

32	48	100.0	75	2 Q8T3D9_CAEEL	Q8T3D9 caenorhabdi
33	48	100.0	76	2 Q9V1H4_DROME	Q9V1H4 drosophila
34	48	100.0	77	2 Q20690_CAEEL	Q20690 caenorhabdi
35	48	100.0	77	2 Q9ZJ18_HELPU	Q9ZJ18 helicobacte
36	48	100.0	80	2 Q61310_CAEER	Q61310 caenorhabdi
37	48	100.0	80	2 Q7JPU3_CAEEL	Q7JPU3 caenorhabdi
38	48	100.0	82	2 Q6IDQ0_CAEER	Q6IDQ0 caenorhabdi
39	48	100.0	83	2 Q20689_CAEEL	Q20689 caenorhabdi
40	48	100.0	84	2 Q615X5_CAEER	Q615X5 caenorhabdi
41	48	100.0	85	2 Q58WZ3_ORENT	Q58WZ3 orochromis
42	48	100.0	86	2 Q5TRG3_ANOGA	Q5TRG3 anopheles g
43	48	100.0	87	2 Q61311_CAEER	Q61311 caenorhabdi
44	48	100.0	87	2 Q61HCE_DROME	Q61HCE drosophila
45	48	100.0	89	2 Q6E1J5_DICDI	Q6E1J5 dictyostei
46	48	100.0	89	2 Q6EPJ7_ORYSA	Q6EPJ7 oryza sativ
47	48	100.0	89	2 Q598K8_AGRXA	Q598K8 agrostodon
48	48	100.0	91	2 Q5Z4U5_ORYSA	Q5Z4U5 oryza sativ
49	48	100.0	92	2 Q18410_CAEEL	Q18410 caenorhabdi
50	48	100.0	93	2 Q6E1J4_DICDI	Q6E1J4 dictyostei
51	48	100.0	94	2 Q5M1V4_ABDAL	Q5M1V4 aedes albop
52	48	100.0	94	2 Q6ND72_RHOPA	Q6ND72 rhodopseudo
53	48	100.0	97	2 Q5M1X7_ABDAL	Q5M1X7 aedes albop
54	48	100.0	101	2 Q5AHK9_CANAL	Q5AHK9 candida alb
55	48	100.0	102	2 Q59QY5_CANAL	Q59QY5 candida alb
56	48	100.0	102	2 Q9VUEL_DROME	Q9VUEL drosophila
57	48	100.0	102	2 Q94189_CAEEL	Q94189 caenorhabdi
58	48	100.0	103	2 Q970X8_SULTO	Q970X8 sulfolobus
59	48	100.0	104	2 Q7PKY4_ANOGA	Q7PKY4 anopheles g
60	48	100.0	104	2 Q6E1K1_DICDI	Q6E1K1 dictyostei
61	48	100.0	104	2 Q46246_S01PT	Q46246 drosophila
62	48	100.0	107	2 Q9VQW5_DROME	Q9VQW5 drosophila
63	48	100.0	108	2 Q5ADL5_CANAL	Q5ADL5 candida alb
64	48	100.0	109	2 Q8MXA9_9ECHAN	Q8MXA9 holopneuste
65	48	100.0	109	2 Q9D6B9_MOUSE	Q9D6B9 mus musculu
66	48	100.0	112	2 Q8MXB0_9ECHAN	Q8MXB0 holopneuste
67	48	100.0	113	2 Q5A9C8_CANAL	Q5A9C8 candida alb
68	48	100.0	113	2 Q5TWL5_ANOGA	Q5TWL5 anopheles g
69	48	100.0	113	2 Q7P100_ANOGA	Q7P100 anopheles g
70	48	100.0	113	2 Q5QL74_ORYSA	Q5QL74 oryza sativ
71	48	100.0	113	2 Q6Z1U5_ORYSA	Q6Z1U5 oryza sativ
72	48	100.0	114	1 AGR2_LYCES	P37219 lycopersico
73	48	100.0	114	2 Q61GR9_DROME	Q61GR9 drosophila
74	48	100.0	114	2 Q40165_LYCES	Q40165 lycopersico
75	48	100.0	114	2 Q7XYV3_LYCES	Q7XYV3 lycopersico
76	48	100.0	114	2 Q7XYV6_LYCES	Q7XYV6 lycopersico
77	48	100.0	114	2 Q7XYV6_LYCCH	Q7XYV6 lycopersico
78	48	100.0	114	2 Q84ZL8_ORYSA	Q84ZL8 oryza sativ
79	48	100.0	115	2 Q9YAJ2_AERPE	Q9YAJ2 aetopyrum p
80	48	100.0	115	2 Q5M1X6_ABDAL	Q5M1X6 aedes albop
81	48	100.0	115	2 Q559F6_DICDI	Q559F6 dictyostei
82	48	100.0	116	2 Q59L13_CANAL	Q59L13 candida alb
83	48	100.0	117	2 Q59U45_CANAL	Q59U45 candida alb
84	48	100.0	117	2 Q67WD5_ORYSA	Q67WD5 oryza sativ
85	48	100.0	118	2 Q60WM5_CAEER	Q60WM5 caenorhabdi
86	48	100.0	118	2 Q7JPP1_CAEEL	Q7JPP1 caenorhabdi
87	48	100.0	119	2 Q59JW6_CANAL	Q59JW6 candida alb
88	48	100.0	119	2 Q938Z7_CAEEL	Q938Z7 caenorhabdi
89	48	100.0	120	2 Q592P7_LYMST	Q592P7 lymanea tra
90	48	100.0	122	2 Q96Z06_SULTO	Q96Z06 sulfolobus
91	48	100.0	122	2 Q23089_ARATH	Q23089 arabidopsis
92	48	100.0	122	2 Q9FJCS_ARATH	Q9FJCS arabidopsis
93	48	100.0	122	2 Q4SXT2_TETNG	Q4SXT2 terradon n
94	48	100.0	123	2 Q54CDS_DICDI	Q54CDS dictyostei
95	48	100.0	124	2 Q5D9C9_SCHJA	Q5D9C9 schistosoma
96	48	100.0	124	2 Q61IKS_DROME	Q61IKS drosophila
97	48	100.0	127	2 Q7QJPE_ANOGA	Q7QJPE anopheles g
98	48	100.0	127	2 Q84LH6_ORYSA	Q84LH6 oryza sativ
99	48	100.0	127	2 Q82ZNA_ENTFA	Q82ZNA enterococcu
100	48	100.0	128	2 Q4JBM7_SULAC	Q4JBM7 sulfolobus
101	48	100.0	132	2 Q59S89_CANAL	Q59S89 candida alb
102	48	100.0	132	2 Q61L47_DROME	Q61L47 drosophila
103	48	100.0	132	2 Q7X1Z6_ORYSA	Q7X1Z6 oryza sativ
104	48	100.0	132	2 Q9XY97_LAMFL	Q9XY97 lampectra fl

105	48	100.0	135	2	Q4TES1_TESTNG	Q4tes1 tetraodon n	178	48	100.0	164	2	Q8N033_9DIPT	Q8n033 drosophila
106	48	100.0	136	2	Q08657_RAT	Q08657 rattus norv	179	48	100.0	164	2	Q6VJ28_ORYSA	Q6vJ28 oryza sativ
107	48	100.0	137	2	Q54KZ0_DICDI	Q54kz0 dictyosteli	180	48	100.0	165	2	Q8N016_9DIPT	Q8n016 drosophila
108	48	100.0	137	2	Q6116_DROME	Q6116 drosophila	181	48	100.0	165	2	Q8N019_9DIPT	Q8n019 drosophila
109	48	100.0	137	2	Q8ENS9_OCRBH	Q8ens9 ocanorbhaci	182	48	100.0	165	2	Q8N022_9DIPT	Q8n022 drosophila
110	48	100.0	138	2	Q4TVN3_SHEEP	Q4tvn3 ovib aries	183	48	100.0	165	2	Q8N024_9DIPT	Q8n024 drosophila
111	48	100.0	138	2	Q4TV04_MALZE	Q4tv04 zea mays (m	184	48	100.0	165	2	Q8N026_9DIPT	Q8n026 drosophila
112	48	100.0	139	2	Q9UAV7_CABEL	Q9uav7 caenorhabdi	185	48	100.0	165	2	Q8N031_DROAV	Q8n031 drosophila
113	48	100.0	140	1	PROF3_WHEAT	P493J3 triticum ae	186	48	100.0	165	2	Q8N034_9DIPT	Q8n034 drosophila
114	48	100.0	140	1	Q26056_PLALO	Q26056 plasmodium	187	48	100.0	165	2	Q6BD24_XENLA	Q6bd24 xenopus lae
115	48	100.0	140	2	Q17821_CABEL	Q17821 caenorhabdi	188	48	100.0	166	2	Q8N021_9DIPT	Q8n021 drosophila
116	48	100.0	140	2	Q8RZM6_ORYSA	Q8rzm6 oryza sativ	189	48	100.0	166	2	Q8N037_9DIPT	Q8n037 drosophila
117	48	100.0	140	2	Q616G5_BRARE	Q616g5 brachydantio	190	48	100.0	166	2	Q617A1_DROME	Q617a1 drosophila
118	48	100.0	140	2	Q4TH05_TESTNG	Q4th05 tetraodon n	191	48	100.0	166	2	Q5XGE4_XENTR	Q5xge4 xenopus tro
119	48	100.0	141	1	PROF2_WHEAT	P493J3 triticum ae	192	48	100.0	166	2	Q61P57_XENLA	Q61p57 xenopus lae
120	48	100.0	141	2	Q6H100_BACHK	Q6h100 bacillus th	193	48	100.0	167	2	Q8N025_DROSR	Q8n025 drosophila
121	48	100.0	141	2	Q63DH7_BACCZ	Q63dh7 bacillus ce	194	48	100.0	167	2	Q8N038_9DIPT	Q8n038 drosophila
122	48	100.0	142	2	Q6NPG2_ARATH	Q6npg2 arabidopsis	195	48	100.0	167	2	Q8N044_9DIPT	Q8n044 drosophila
123	48	100.0	142	2	Q81FM0_BACCR	Q81fm0 bacillus ce	196	48	100.0	167	2	Q8N057_DROAI	Q8n057 drosophila
124	48	100.0	142	2	Q8U216_PPAPI	Q8u216 phocoena sp	197	48	100.0	167	2	O17346_CABEL	O17346 caenorhabdi
125	48	100.0	143	1	CB1X_METUA	Q8u380 mechanococ	198	48	100.0	168	2	Q7FX82_ANOGA	Q7fx82 anopheles g
126	48	100.0	143	1	CB1X_METKA	Q8cy77 mechanopyru	199	48	100.0	168	2	Q8N018_9DIPT	Q8n018 drosophila
127	48	100.0	143	2	Q615Y1_CABER	Q615y1 caenorhabdi	200	48	100.0	169	2	Q61H82_CABER	Q61h82 caenorhabdi
128	48	100.0	143	2	Q86N07_DROME	Q86nq7 drosophila	201	48	100.0	169	2	Q8N055_DROTO	Q8n055 drosophila
129	48	100.0	144	1	CB1X_METNP	P61919 mechanococ	202	48	100.0	169	2	Q8N058_DROPS	Q8n058 drosophila
130	48	100.0	145	2	Q59LJ7_CANAL	Q59lj7 candida alb	203	48	100.0	169	2	Q8N059_DROPE	Q8n059 drosophila
131	48	100.0	145	2	Q31510_BACSU	Q31510 bacillus su	204	48	100.0	169	2	Q8N060_DROAM	Q8n060 drosophila
132	48	100.0	145	2	Q90ZQ7_ORYLA	Q90zq7 oryzae lat	205	48	100.0	170	2	Q7SGJ3_NEUCR	Q7sgj3 neurospora
133	48	100.0	146	2	Q91891_CHICK	Q91891 gallus gall	206	48	100.0	171	2	Q5Y998_CANAL	Q5y998 candida alb
134	48	100.0	146	2	Q4RCM5_TESTNG	Q4rcm5 tetraodon n	207	48	100.0	172	2	Q8N056_DROBF	Q8n056 drosophila
135	48	100.0	147	2	Q5TXJ7_ANOGA	Q5txj7 anopheles g	208	48	100.0	172	2	Q502A3_BRARE	Q502a3 brachydantio
136	48	100.0	148	2	Q6BW81_DESHA	Q6bw81 debaryomyce	209	48	100.0	173	2	Q5Y143_CANAL	Q5y143 candida alb
137	48	100.0	148	1	Q61D46_9MURI	Q61d46 rattus sp.	210	48	100.0	174	2	Q5E280_VIBF1	Q5e280 vibrio fisc
138	48	100.0	149	1	Q8399B_DROME	Q9v16 drosophila	211	48	100.0	174	2	Q951E0_CANFA	Q951e0 canis famli
139	48	100.0	152	2	Q8N014_DROEL	Q8n014 drosophila	212	48	100.0	176	2	Q81A55_CABEL	Q81a55 caenorhabdi
140	48	100.0	152	2	Q8N052_DROTK	Q8n052 drosophila	213	48	100.0	176	2	Q91Z58_ARATH	Q91z58 arabidopsis
141	48	100.0	153	2	Q8N050_9DIPT	Q8n050 drosophila	214	48	100.0	178	2	Q91TP2_ARATH	Q91tp2 arabidopsis
142	48	100.0	154	2	Q8N041_DROEU	Q8n041 drosophila	215	48	100.0	181	2	Q61K24_DROME	Q61k24 drosophila
143	48	100.0	154	2	Q8N048_9DIPT	Q8n048 drosophila	216	48	100.0	183	2	Q5DEJ0_SCHJA	Q5dej0 schistosoma
144	48	100.0	154	2	Q8N051_DROLT	Q8n051 drosophila	217	48	100.0	183	2	Q5Z8B9_ORYSA	Q5z8b9 oryza sativ
145	48	100.0	155	2	Q8N031_DROFC	Q8n031 drosophila	218	48	100.0	185	2	O00837_LEIBR	O00837 leishmania
146	48	100.0	155	2	Q8N039_DROVA	Q8n039 drosophila	219	48	100.0	185	2	Q4RFA5_TESTNG	Q4rfa5 tetraodon n
147	48	100.0	155	2	Q8N040_DROTE	Q8n040 drosophila	220	48	100.0	187	2	Q6N1E5_ARATH	Q6n1e5 arabidopsis
148	48	100.0	155	2	Q8N042_9DIPT	Q8n042 drosophila	221	48	100.0	188	2	Q5AF41_CANAL	Q5af41 candida alb
149	48	100.0	155	2	Q8N047_DROAN	Q8n047 drosophila	222	48	100.0	188	2	Q61HRE_DROME	Q61hre drosophila
150	48	100.0	156	2	Q8N053_9DIPT	Q8n053 drosophila	223	48	100.0	191	2	Q59N16_CANAL	Q59n16 candida alb
151	48	100.0	157	2	Q8N043_9DIPT	Q8n043 drosophila	224	48	100.0	191	2	Q61KE7_DROME	Q61ke7 drosophila
152	48	100.0	157	2	Q8N045_9DIPT	Q8n045 drosophila	225	48	100.0	192	2	Q56WX8_ORENI	Q56wx8 oreochromis
153	48	100.0	157	2	Q8N049_9DIPT	Q8n049 drosophila	226	48	100.0	192	1	HUNB_DROAD	HUNB_DROAD
154	48	100.0	157	2	Q8N054_9DIPT	Q8n054 drosophila	227	48	100.0	192	1	HUNB_DROTA	HUNB_DROTA
155	48	100.0	157	2	Q9PVJ2_CHATV	Q9pvj2 charina tri	228	48	100.0	193	1	HUNB_DROIK	HUNB_DROIK
156	48	100.0	158	1	HUNB_DROMM	Q46z48 drosophila	229	48	100.0	193	2	Q7QIH3_ANOGA	Q7qih3 anopheles g
157	48	100.0	158	1	Q94577_HELER	Q94577 helicodactyl	230	48	100.0	195	1	HUNB_DROPA	HUNB_DROPA
158	48	100.0	159	1	HUNB_DROSO	Q46z58 drosophila	231	48	100.0	196	1	HUNB_DROXA	HUNB_DROXA
159	48	100.0	159	2	Q9YMT6_NPVLD	Q9ymt6 lymantria d	232	48	100.0	196	1	HUNB_DROSL	HUNB_DROSL
160	48	100.0	159	2	Q8JIL5_9CICH	Q8jil5 ascatocliap	233	48	100.0	196	2	Q7P114_ANOGA	Q7p114 anopheles g
161	48	100.0	159	2	Q8JIL6_ASTATL	Q8jil6 ascatoecoch	234	48	100.0	197	2	Q61LFI_DROME	Q61lfi drosophila
162	48	100.0	159	2	Q8JIL7_9CICH	Q8jil7 trophus du	235	48	100.0	197	2	Q94F76_MALZE	Q94f76 zea mays (m
163	48	100.0	159	2	Q8JIL8_9CICH	Q8jil8 labidochrom	236	48	100.0	198	1	HUNB_DROCY	HUNB_DROCY
164	48	100.0	160	2	Q8N046_DROVA	Q8n046 drosophila	237	48	100.0	198	1	HUNB_DRODS	HUNB_DRODS
165	48	100.0	161	2	Q8N015_DROEC	Q8n015 drosophila	238	48	100.0	198	1	HUNB_DROLI	HUNB_DROLI
166	48	100.0	161	2	Q8N030_9DIPT	Q8n030 drosophila	239	48	100.0	198	2	Q61KX1_DROME	Q61kx1 drosophila
167	48	100.0	161	2	Q54YM7_DICDI	Q54ym7 dictyosteli	240	48	100.0	198	2	Q7XQSO_ORYSA	Q7xqso oryza sativ
168	48	100.0	162	2	Q8N020_9DIPT	Q8n020 drosophila	241	48	100.0	198	2	Q614M2_ORYSA	Q614m2 oryza sativ
169	48	100.0	162	2	Q8N035_DROPN	Q8n035 drosophila	242	48	100.0	199	2	Q61GJ3_DROME	Q61gj3 drosophila
170	48	100.0	163	2	Q8N017_9DIPT	Q8n017 drosophila	243	48	100.0	199	2	Q6YUUS_ORYSA	Q6yuus oryza sativ
171	48	100.0	163	2	Q8N036_9DIPT	Q8n036 drosophila	244	48	100.0	199	2	Q751R7_ORYSA	Q751r7 oryza sativ
172	48	100.0	163	2	Q7YTA3_9MYRI	Q7yta3 glomeris ma	245	48	100.0	200	2	Q61WN4_BRARE	Q61wn4 brachiolesto
173	48	100.0	164	2	Q8N023_DROTS	Q8n023 drosophila	246	48	100.0	200	2	Q7Q0Z7_ANOGA	Q7q0z7 anopheles g
174	48	100.0	164	2	Q8N027_DROLN	Q8n027 drosophila	247	48	100.0	200	2	Q4STZ9_TESTNG	Q4stz9 tetraodon n
175	48	100.0	164	2	Q8N028_DROKI	Q8n028 drosophila	248	48	100.0	201	2	Q4R176_CABEL	Q4r176 caenorhabdi
176	48	100.0	164	2	Q8N029_9DIPT	Q8n029 drosophila	249	48	100.0	202	1	HAND1_CHICK	HAND1 gallus gall
177	48	100.0	164	2	Q8N032_9DIPT	Q8n032 drosophila	250	48	100.0	202	2	Q6AV25_ORYSA	Q6av25 oryza sativ

251	48	100.0	203	2	Q7S411_NEUCR	Q7S411_neutrospora	324	48	100.0	235	2	Q76647_CABEL	Q76647_caenorhabdi
252	48	100.0	203	2	Q6S2S4_HUMAN	Q6S2S4_homo sapien	325	48	100.0	235	2	Q7X8E2_ORYSA	Q7X8E2_oryza sativ
253	48	100.0	204	1	HAND1_SHEEP	O28E55 ovis aries	326	48	100.0	235	2	Q6QPY7_MIMRI	Q6QPY7_mimulus rin
254	48	100.0	206	2	Q4S86E_CABEL	O4S868 caenorhabdi	327	48	100.0	236	2	Q4MMU8_ASPFU	Q4MMU8_aspergillus
255	48	100.0	207	2	Q5TYI3_BRARE	O5TYI3_brachydanio	328	48	100.0	236	2	Q5T0S5_ANOGA	O5T0S5_anopheles g
256	48	100.0	208	2	Q9NFP3_LEIMA	O9NFP3_leishmania	329	48	100.0	236	2	O6L1T5_CAEBR	O6L1T5_caenorhabdi
257	48	100.0	208	2	Q6IGL9_DROME	O6IGL9_drosophila	330	48	100.0	236	2	Q7XPC7_ORYSA	Q7XPC7_oryza sativ
258	48	100.0	208	2	Q221S6_CABEL	O221S6_caenorhabdi	331	48	100.0	236	2	Q9QWE1_9MURI	Q9QWE1_mus sp. cia
259	48	100.0	209	2	Q5CPB5_CRYPV	O5CPB5_cryptospori	332	48	100.0	237	2	Q6QVX6_MIMGU	Q6QVX6_mimulus gut
260	48	100.0	209	2	Q5S8Z0_DICDI	O5S8Z0_dictyosteli	333	48	100.0	238	2	O8C173_MOUSE	O8C173_mus musculi
261	48	100.0	212	2	Q564Y0_CABEL	O564Y0_caenorhabdi	334	48	100.0	239	1	CU058_HUMAN	P58305_homo sapien
262	48	100.0	212	2	Q6RYE6_TRTMO	O6RYE6_citricum tu	335	48	100.0	239	2	Q9STB3_DROME	Q9STB3_drosophila
263	48	100.0	212	2	Q6RYE6_TRTMO	O6RYE6_citricum tu	336	48	100.0	239	2	Q721G6_TRYCR	Q721G6_trypanosoma
264	48	100.0	212	2	Q6RY79_TRTMO	O6RY79_citricum mo	337	48	100.0	240	2	Q9LMP5_ARATH	Q9LMP5_arabidopsis
265	48	100.0	213	2	Q6RY74_TRTMO	O6RY74_citricum mo	338	48	100.0	240	2	P84136_BACST	P84136_bacillus st
266	48	100.0	213	2	Q6RY76_TRTMO	O6RY76_citricum mo	339	48	100.0	241	2	O54EB4_DICDI	O54EB4_dictyosteli
267	48	100.0	213	2	Q6RY77_TRTMO	O6RY77_citricum mo	340	48	100.0	242	2	Q9VYW4_DROME	Q9VYW4_drosophila
268	48	100.0	213	2	Q6RYE4_TRTMO	O6RYE4_citricum mo	341	48	100.0	242	2	Q4WT78_ASPFU	Q4WT78_aspergillus
269	48	100.0	213	2	Q6S6M0_9MAGN	O6S6M0_nymphaea sp	342	48	100.0	242	2	Q9N3Z0_CABEL	Q9N3Z0_caenorhabdi
270	48	100.0	213	2	Q6N613_RHOPA	O6N613_rhodopseudo	343	48	100.0	242	2	O8LRJ3_ORYSA	O8LRJ3_oryza sativ
271	48	100.0	214	2	Q5TVW8_ANOGA	O5TVW8_anopheles g	344	48	100.0	242	2	Q6QVY0_SALCC	Q6QVY0_salvia coc
272	48	100.0	214	2	Q6RY65_HORYU	O6RY65_hordeum vul	345	48	100.0	242	2	O5B8Y3_ORENI	O5B8Y3_oreochromis
273	48	100.0	214	2	Q6QVY5_PAUTO	O6QVY5_paulownia t	346	48	100.0	243	2	Q9P2R2_HUMAN	Q9P2R2_homo sapien
274	48	100.0	215	1	HAND1_HUMAN	O96004_homo sapien	347	48	100.0	243	2	Q9N2G1_PONPY	Q9N2G1_pongo pygma
275	48	100.0	215	1	HAND1_RABIT	P57100_oryctolagus	348	48	100.0	243	2	Q9N2G2_PPRIM	Q9N2G2_gorilla gor
276	48	100.0	216	1	HAND1_MOUSE	O64279_m heart - an	349	48	100.0	243	2	Q9N2G3_PANTR	Q9N2G3_pan troglod
277	48	100.0	216	1	HAND1_MOUSE	P97832_rattus norv	350	48	100.0	243	2	Q7TQW2_MOUSE	Q7TQW2_mus musculi
278	48	100.0	216	2	Q8N7N5_HUMAN	O8N7N5_homo sapien	351	48	100.0	244	2	Q6Q3M4_9PIPT	Q6Q3M4_9pipt
279	48	100.0	216	2	Q5SQG1_MOUSE	O5SQG1_mus musculi	352	48	100.0	244	2	Q8UHA3_CHICK	Q8UHA3_chick
280	48	100.0	216	2	Q8OUL7_MOUSE	O8OUL7_mus musculi	353	48	100.0	245	2	Q4WSR3_ORYSA	Q4WSR3_oryza sativ
281	48	100.0	216	2	Q4V8L8_RAT	O4V8L8_rattus norv	354	48	100.0	245	2	O54125_DICDI	O54125_dictyosteli
282	48	100.0	216	2	Q9W7C7_ORYIA	O9W7C7_oryzias lat	355	48	100.0	246	2	O5L1H3_ORYSA	O5L1H3_oryza sativ
283	48	100.0	217	1	ATL2I1_ARATH	O8RXZ2_arabidopsis	356	48	100.0	247	2	O5ABO8_CANAL	O5ABO8_candida alb
284	48	100.0	217	2	Q7Q13B_ANOGA	O7Q138_anopheles g	357	48	100.0	247	2	Q7PEFX_ANOGA	Q7PEFX_anopheles g
285	48	100.0	217	2	Q51SL6_MACFA	O51S16_macaca fasc	358	48	100.0	247	2	Q5BPF0_ARATH	Q5BPF0_arabidopsis
286	48	100.0	217	2	Q58L58_PIG	O58L58_sus scrofa	359	48	100.0	248	2	Q6K5X1_ORYSA	Q6K5X1_oryza sativ
287	48	100.0	218	2	Q754W7_ASHGO	O754W7_asbysa goss	360	48	100.0	249	2	Q75K45_ORYSA	Q75K45_oryza sativ
288	48	100.0	219	1	Q6OVX7_MIMLE	O6OVX7_mimulus lew	361	48	100.0	250	2	Q8BKX7_MOUSE	Q8BKX7_mus musculi
289	48	100.0	219	1	MTBM_DROVA	P83733_drosophila	362	48	100.0	250	2	Q7PWE5_ANOGA	Q7PWE5_anopheles g
290	48	100.0	219	2	Q5TRN0_ANOGA	O5TRN0_anopheles g	363	48	100.0	252	2	Q6QPY8_MAZRE	Q6QPY8_mazus rept
291	48	100.0	219	2	Q9VDW8_DROME	O9VDW8_drosophila	364	48	100.0	254	2	Q9V582_DROME	Q9V582_drosophila
292	48	100.0	219	2	P83699_BACST	O83699_bacillus st	365	48	100.0	254	2	Q4RNP8_TETNG	Q4RNP8_tetradodon n
293	48	100.0	219	2	O55579_NPYTS	O55579_leucania se	366	48	100.0	255	2	Q6KBO5_MOUSE	Q6KBO5_mus musculi
294	48	100.0	220	2	Q7S6T5_NEUCR	O7S6T5_neutrospora	367	48	100.0	255	2	Q7RWY3_NEUCR	Q7RWY3_neutrospora
295	48	100.0	220	2	O557E5_DICDI	O557E5_dictyosteli	368	48	100.0	256	2	O13722_HUMAN	O13722_homo sapien
296	48	100.0	220	2	Q86HZ5_DICDI	O86HZ5_dictyosteli	369	48	100.0	256	2	Q6S3X1_ORYSA	Q6S3X1_oryza sativ
297	48	100.0	221	2	O5XJN5_BRARE	O5XJN5_brachydanio	370	48	100.0	256	2	Q7XD98_ORYSA	Q7XD98_oryza sativ
298	48	100.0	224	2	Q6WGU1_TRTRE	O6WGU1_trichoderma	371	48	100.0	256	2	Q8W365_ORYSA	Q8W365_oryza sativ
299	48	100.0	224	2	Q4WPH8_ASPFU	O4WPH8_aspergillus	372	48	100.0	259	2	Q7SSM0_ORYSA	Q7SSM0_oryza sativ
300	48	100.0	224	2	Q9N9W1_HAIRO	O9N9W1_haloerythra	373	48	100.0	259	2	O5CPB3_CRYPV	O5CPB3_cryptospori
301	48	100.0	224	2	Q9N9W2_HAIRO	O9N9W2_haloerythra	374	48	100.0	259	2	O9V7K6_DROME	O9V7K6_drosophila
302	48	100.0	225	2	Q7XZF0_ORYSA	O7XZF0_oryza sativ	375	48	100.0	259	2	O9SA48_ARATH	O9SA48_arabidopsis
303	48	100.0	225	2	Q6QPY1_MIMKE	O6QPY1_mimulus kel	376	48	100.0	259	2	Q9ZTC8_ARATH	Q9ZTC8_arabidopsis
304	48	100.0	225	2	Q90XZ3_ERPCA	O90XZ3_erythrochh	377	48	100.0	259	2	O66901_AQUAE	O66901_aquilex aeo
305	48	100.0	225	2	Q4RVT9_TETNG	O4RVT9_tetradodon n	378	48	100.0	259	2	Q7T1L0_9SMEG	Q7T1L0_odontesthes
306	48	100.0	226	2	Q9QZD2_RAT	O9QZD2_rattus norv	379	48	100.0	260	2	Q9ST44_DROME	Q9ST44_drosophila
307	48	100.0	227	2	Q6QPY2_9LAMI	O6QPY2_leucocarpus	380	48	100.0	261	2	O4SGT5_TETNG	O4SGT5_tetradodon n
308	48	100.0	229	2	Q7PIS3_ANOGA	O7PIS3_anopheles g	381	48	100.0	263	2	Q9ARB0_FLATR	Q9ARB0_floverita tr
309	48	100.0	229	2	Q6S124_9MAGN	O6S124_dicentra ex	382	48	100.0	267	2	Q7SE09_NEUCR	Q7SE09_neutrospora
310	48	100.0	230	2	Q7S263_HUMAN	O7S263_homo sapien	383	48	100.0	268	2	O59VW7_CANAL	O59VW7_candida alb
311	48	100.0	230	2	O5CPB6_CRYPV	O5CPB6_cryptospori	384	48	100.0	268	2	Q7S806_HUMAN	Q7S806_homo sapien
312	48	100.0	230	2	Q7RDM4_PLAYO	O7RDM4_plasmodium	385	48	100.0	268	2	O5CVU3_CRYPV	O5CVU3_cryptospori
313	48	100.0	230	2	Q6ZCM4_ORYSA	O6ZCM4_oryza sativ	386	48	100.0	268	2	O5RQW6_ARATH	O5RQW6_anopheles g
314	48	100.0	230	2	Q9M205_ARATH	O9M205_arabidopsis	387	48	100.0	268	2	Q9HAX7_DICDI	Q9HAX7_dictyosteli
315	48	100.0	231	2	Q81QK7_DROME	O81QK7_drosophila	388	48	100.0	269	2	Q9LPF4_ARATH	Q9LPF4_arabidopsis
316	48	100.0	232	2	Q7S3F2_NEUCR	O7S3F2_neutrospora	389	48	100.0	270	2	O9FFC6_ARATH	O9FFC6_arabidopsis
317	48	100.0	232	2	Q7PY53_ANOGA	O7PY53_anopheles g	390	48	100.0	271	1	HMB_XENLA	O5C1T2_schistosoma
318	48	100.0	233	2	O8TC53_HUMAN	O8TC53_homo sapien	391	48	100.0	271	2	O5C1T2_SCHJA	P14837_xenopus lae
319	48	100.0	233	2	O6PIU3_HUMAN	O6PIU3_homo sapien	392	48	100.0	271	2	O4H2U1_CLOIN	O4H2U1_ciona intes
320	48	100.0	233	2	O8MP30_DICDI	O8MP30_dictyosteli	393	48	100.0	271	2	O84WK2_ARATH	O84WK2_arabidopsis
321	48	100.0	233	2	Q7XTV6_ORYSA	Q7XTV6_oryza sativ	394	48	100.0	271	2	O5VR71_ORYSA	O5VR71_oryza sativ
322	48	100.0	234	2	O8STF5_DICDI	O8STF5_dictyosteli	395	48	100.0	272	1	HXAP_HUMAN	P31269_homo sapien
323	48	100.0	234	2	O551Q1_DICDI	O551Q1_dictyosteli	396	48	100.0	272	2	O5CMT6_CRYHO	O5CMT6_cryptospori

397	48	100.0	273	2	0540Y5	DICDI	0540Y5	dictyosteli	470	48	100.0	305	2	091346	XENLA	091346	xenopus lae
398	48	100.0	273	2	04T2H7	TEING	04T2H7	tetradon n	471	48	100.0	306	1	PRRT1	HUMAN	099946	homo sapien
399	48	100.0	274	2	09XGS2	SOYBN	09XGS2	glycine max	472	48	100.0	306	1	PRRT1	MOUSE	035449	mus musculus
400	48	100.0	274	2	05KYZ7	GEOKA	05KYZ7	geobacillus	473	48	100.0	306	2	054CU2	DICDI	054CU2	dictyosteli
401	48	100.0	275	2	05KFEV8	CRNE	05KFEV8	crptococcu	474	48	100.0	306	2	08LH59	ORYSA	08LH59	oryza sativ
402	48	100.0	275	2	055QAB	CRNE	055QAB	crptococcu	475	48	100.0	307	1	YK55	YEAST	YK55	saccharomyc
403	48	100.0	275	2	064700	ARATH	064700	arabidopsi	476	48	100.0	307	2	075H63	ORYSA	075H63	oryza sativ
404	48	100.0	276	2	04R946	MACFA	04R946	macaca fasc	477	48	100.0	308	2	054G56	DICDI	054G56	dictyosteli
405	48	100.0	276	2	09DGB3	LAMJA	09DGB3	lampetra ja	478	48	100.0	308	2	067168	AQUAE	067168	aquilex aeo
406	48	100.0	276	2	P79788	CHICK	P79788	gallus gall	479	48	100.0	308	2	06GBE3	STRAAS	06GBE3	staphylococ
407	48	100.0	277	2	05A4K1	CANAL	05A4K1	candida alb	480	48	100.0	308	2	06GIV5	STRAAR	06GIV5	staphylococ
408	48	100.0	277	2	04PHR7	USMA	04PHR7	urelilago ma	481	48	100.0	308	2	05MHY1	STRAAC	05MHY1	staphylococ
409	48	100.0	277	2	0652W5	ORYSA	0652W5	oryza sativ	482	48	100.0	308	2	07A6X1	STRAAN	07A6X1	staphylococ
410	48	100.0	277	2	04S3L7	TEING	04S3L7	tetradon n	483	48	100.0	308	2	08BXQ1	STRAAM	08BXQ1	staphylococ
411	48	100.0	277	2	04VQD4	GASAC	04VQD4	gaasteroste	484	48	100.0	308	2	099VT4	STRAAM	099VT4	staphylococ
412	48	100.0	278	2	08LEB5	ARATH	08LEB5	arabidopsi	485	48	100.0	309	2	05DHK3	SCJHA	05DHK3	schistosoma
413	48	100.0	278	2	094EJ7	MAIZE	094EJ7	zea mays (m	486	48	100.0	309	2	018751	CABEL	018751	caenorhabdi
414	48	100.0	279	2	065XEB	ORYSA	065XEB	oryza sativ	487	48	100.0	309	2	084ME6	ORYSA	084ME6	oryza sativ
415	48	100.0	279	2	04RA01	TEING	04RA01	tetradon n	488	48	100.0	311	2	06B4W5	DEBHA	06B4W5	debatyomyc
416	48	100.0	280	2	057217	PTTYP	057217	trypanosoma	489	48	100.0	311	2	08H077	ORYSA	08H077	oryza sativ
417	48	100.0	280	2	09AR63	SOLTU	09AR63	soilann tub	490	48	100.0	311	2	090370	COTJA	090370	coturnix co
418	48	100.0	283	2	05JK41	ORYSA	05JK41	oryza sativ	491	48	100.0	311	2	090888	CHICK	090888	gallus gall
419	48	100.0	285	2	082166	ARATH	082166	arabidopsi	492	48	100.0	312	2	081RR4	DROME	081RR4	drone
420	48	100.0	285	2	09LGP3	ORYSA	09LGP3	oryza sativ	493	48	100.0	312	2	08LHP0	ARATH	08LHP0	arabidopsi
421	48	100.0	285	2	09L534	ARATH	09L534	arabidopsi	494	48	100.0	312	2	06T150	BRARE	06T150	brachydantio
422	48	100.0	286	2	042290	CHICK	042290	gallus gall	495	48	100.0	313	2	06DBE4	XENLA	06DBE4	xenopus lae
423	48	100.0	286	2	057342	COTJA	057342	coturnix co	496	48	100.0	313	2	09PUA6	XENLA	09PUA6	xenopus lae
424	48	100.0	286	2	08AMH8	CHICK	08AMH8	gallus gall	497	48	100.0	313	2	04RNI4	TEING	04RNI4	tetradon n
425	48	100.0	286	2	04RM07	TEING	04RM07	tetradon n	498	48	100.0	314	2	09SPJ7	GOSHI	09SPJ7	goshyplum h
426	48	100.0	288	2	052AN2	MAGCR	052AN2	magnaporthe	499	48	100.0	314	2	09M9A3	ARATH	09M9A3	arabidopsi
427	48	100.0	288	2	07PPD2	ANOGA	07PPD2	anopheles g	500	48	100.0	314	2	04S508	TEING	04S508	tetradon n
428	48	100.0	288	2	08RTA39	HERGL	08RTA39	heterodera	501	48	100.0	315	2	08LT06	ORYSA	08LT06	oryza sativ
429	48	100.0	289	2	07XV64	XENTR	07XV64	xenopus tro	502	48	100.0	315	2	0512G4	GEOKA	0512G4	geobacillus
430	48	100.0	289	2	04UIU2	XENTR	04UIU2	xenopus tro	503	48	100.0	315	2	098UK3	BRARE	098UK3	brachydantio
431	48	100.0	290	2	086P14	DROME	086P14	drosophila	504	48	100.0	316	2	06K6C4	ORYSA	06K6C4	oryza sativ
432	48	100.0	290	2	045456	CABEL	045456	caenorhabdi	505	48	100.0	316	2	0504L8	XENTR	0504L8	xenopus tro
433	48	100.0	290	2	06ZGY7	ORYSA	06ZGY7	oryza sativ	506	48	100.0	317	2	05UJPT	ORYSA	05UJPT	oryza sativ
434	48	100.0	292	2	06YUV0	ORYSA	06YUV0	oryza sativ	507	48	100.0	317	2	06P4L0	XENTR	06P4L0	xenopus tro
435	48	100.0	292	2	0857E3	ORYSA	0857E3	oryza sativ	508	48	100.0	317	2	07SA92	NEUCR	07SA92	neurospora
436	48	100.0	292	2	07XC01	ORYSA	07XC01	oryza sativ	509	48	100.0	318	2	04GYV8	PTTYP	04GYV8	trypanosoma
437	48	100.0	292	2	05QZB8	IDIL0	05QZB8	idiomatina	510	48	100.0	318	2	08H301	ORYSA	08H301	oryza sativ
438	48	100.0	292	2	091294	RANCA	091294	rana catesb	511	48	100.0	318	2	08S026	ORYSA	08S026	oryza sativ
439	48	100.0	294	2	05TRH1	ORYSA	05TRH1	oryza sativ	512	48	100.0	318	2	06NBS6	RHOA	06NBS6	rhodospendo
440	48	100.0	294	2	P94395	BACSU	P94395	baacillus su	513	48	100.0	318	2	06XZHO	BRARE	06XZHO	brachydantio
441	48	100.0	295	2	054CT9	DICDI	054CT9	dictyosteli	514	48	100.0	319	2	0504T7	HUMAN	0504T7	homo sapien
442	48	100.0	295	2	08SMU6	DROME	08SMU6	drosophila	515	48	100.0	320	2	07PDB9	ANOGA	07PDB9	anopheles g
443	48	100.0	296	2	09SSA2	ARATH	09SSA2	arabidopsi	516	48	100.0	320	2	05LTM6	SIILPO	05LTM6	silicibacte
444	48	100.0	297	2	05A295	CANAL	05A295	candida alb	517	48	100.0	320	2	09KCO0	BACHD	09KCO0	baacillus ha
445	48	100.0	297	2	041122	PHAVU	041122	phaseolus v	518	48	100.0	320	2	06STNR2	ANOGA	06STNR2	anopheles g
446	48	100.0	297	2	0627B6	ORYSA	0627B6	oryza sativ	519	48	100.0	321	2	06K5Y1	ORYSA	06K5Y1	oryza sativ
447	48	100.0	297	2	08B2C7	MOUSE	08B2C7	mus musculu	520	48	100.0	321	2	06YX13	ORYSA	06YX13	oryza sativ
448	48	100.0	298	1	MEOX2	XENLA	MEOX2	xenopus lae	521	48	100.0	321	2	023891	ORYSA	023891	oryza sativ
449	48	100.0	298	2	06IKF0	DROME	06IKF0	drosophila	522	48	100.0	321	2	07MU57	PORGI	07MU57	porphyromon
450	48	100.0	298	2	07ZX12	XENLA	07ZX12	xenopus lae	523	48	100.0	321	2	07S197	PRABE	07S197	plasmodium
451	48	100.0	299	2	05TFG4	ANOGA	05TFG4	anopheles g	524	48	100.0	322	2	06ZKS4	ORYSA	06ZKS4	oryza sativ
452	48	100.0	299	2	05LV18	SIILPO	05LV18	silicibacte	525	48	100.0	322	1	MAFB	MOUSE	09Y5Q3	homo sapien
453	48	100.0	300	2	06K722	ORYSA	06K722	oryza sativ	526	48	100.0	323	1	MAFB	MOUSE	P54481	mus musculu
454	48	100.0	300	2	06WGB2	RAT	06WGB2	rattus nov	527	48	100.0	323	1	MAFB	MOUSE	P54842	mus musculu
455	48	100.0	301	2	0656T1	ORYSA	0656T1	oryza sativ	528	48	100.0	323	1	ORX1	BRARE	091994	brachydantio
456	48	100.0	302	1	HYPB	BRATA	054X50	birdytriazib	529	48	100.0	323	1	ORX1	BRARE	091994	brachydantio
457	48	100.0	302	1	054XK0	DICDI	054XK0	dictyosteli	530	48	100.0	323	2	096835	DROME	096835	drosophila
458	48	100.0	302	2	090YH7	CHICK	P50222	gallus gall	531	48	100.0	323	2	09SDW0	ARATH	09SDW0	arabidopsi
459	48	100.0	303	1	MEOX2	HUMAN	P50222	homo sapien	532	48	100.0	323	2	04ST17	TEING	04ST17	tetradon n
460	48	100.0	303	1	MEOX2	MOUSE	P39020	mus musculu	533	48	100.0	324	2	07ZU54	BRARE	07ZU54	brachydantio
461	48	100.0	303	1	MEOX2	RAT	P39020	rattus nov	534	48	100.0	324	2	0756L9	ASHGO	0756L9	ashbya gosb
462	48	100.0	303	2	06FHYE	HUMAN	06FHYE	homo sapien	535	48	100.0	324	2	07X6C5	ORYSA	07X6C5	oryza sativ
463	48	100.0	303	2	095JAB	PIG	095JAB	sus scrofa	536	48	100.0	324	2	06R077	ARATH	06R077	arabidopsi
464	48	100.0	303	2	0544T6	MOUSE	0544T6	mus musculu	537	48	100.0	324	2	09M0Y5	ARATH	09M0Y5	arabidopsi
465	48	100.0	303	2	099M23	MOUSE	099M23	mus musculu	538	48	100.0	324	2	09W6B1	BRARE	09W6B1	brachydantio
466	48	100.0	303	2	04SAL9	TEING	04SAL9	tetradon n	539	48	100.0	325	2	09BSNO	HUMAN	09BSNO	homo sapien
467	48	100.0	304	1	GSH2	HUMAN	09bhm3	homo sapien	540	48	100.0	325	1	06KZW9	BRARE	06KZW9	brachydantio
468	48	100.0	304	1	OS1LC5	MAGCR	OS1LC5	magnaporthe	541	48	100.0	326	1	PTRX2	XENLA	09pwr3	xenopus lae
469	48	100.0	305	1	GSH2	MOUSE	P31316	mus musculu	542	48	100.0	326	2	OTXTU3	ORYSA	07XUC3	oryza sativ

543	48	100.0	326	2	Q91447_PSEAE	Q91447_pseudomonas	616	48	100.0	352	2	Q6NHW3_HUMAN	Q6NHw3_homo sapien
544	48	100.0	326	2	Q90W66_GROBI	Q90w66_brecksario	617	48	100.0	352	2	Q5QLF4_ORYSA	Q5qlf4_oryza sativ
545	48	100.0	327	2	Q98UK4_BRABE	Q98uk4_briachydantio	618	48	100.0	352	2	Q8BDP0_SYNEA	Q8bdp0_synecococc
546	48	100.0	328	1	DLX2_HUMAN	DLX2787_homo sapien	619	48	100.0	353	2	Q4T358_TETNG	Q4t358_tetradon n
547	48	100.0	328	1	ORY1_YEAST	P38271_baccharomyc	620	48	100.0	354	1	QTX1_HUMAN	P32242_homo sapien
548	48	100.0	328	2	Q53QV0_HUMAN	Q53qv0_homo sapien	621	48	100.0	354	2	Q3JTG6_HUMAN	Q3jtg6_homo sapien
549	48	100.0	328	2	Q5VQ11_ORYSA	Q5vq11_oryza sativ	622	48	100.0	354	2	Q54DD6_DICDI	Q54dd6_dicystostei
550	48	100.0	329	2	Q6ZU00_BACLD	Q6zu00_bacillus 1i	623	48	100.0	354	2	Q51M44_DICDI	Q51m44_dicystostei
551	48	100.0	329	2	Q8N1Y1_NEUCR	Q8n1y1_neurospora	624	48	100.0	355	1	OTX1_MOUSE	P80205_mus muscu
552	48	100.0	329	2	Q45N27_ARATH	Q45n27_arabidopsis	625	48	100.0	355	1	OTX1_RAT	Q64140_rattus norv
553	48	100.0	329	2	Q80ZK3_MOUSE	Q80zk3_mus muscu	626	48	100.0	355	2	Q9W481_DROME	Q9w481_drosophila
554	48	100.0	330	2	Q5CEA1_CRYHO	Q5cea1_cryptospori	627	48	100.0	355	2	Q9S7W5_ARATH	Q9s7w5_arabidopsis
555	48	100.0	330	2	Q7XEZ4_ORYSA	Q7xez4_oryza sativ	628	48	100.0	355	2	Q91ZU3_MOUSE	Q91zj3_mus muscu
556	48	100.0	330	2	Q65JD7_BACLD	Q65jd7_bacillus 1i	629	48	100.0	356	2	Q5SS54_MOUSE	Q5ss54_mus muscu
557	48	100.0	331	1	HXA1_MOUSE	P09022_mus muscu	630	48	100.0	356	2	Q5ATR4_ORYSA	Q5atr4_oryza sativ
558	48	100.0	331	2	Q6K5X2_ORYSA	Q6k5x2_oryza sativ	631	48	100.0	356	2	Q9LZFT_ARATH	Q9lzf7_arabidopsis
559	48	100.0	331	2	Q4KSV9_9NUCL	Q4ksv9_chrysodeixi	632	48	100.0	356	2	Q73679_BRABE	Q73679_briachydantio
560	48	100.0	332	1	DLX2_MOUSE	P40764_mus muscu	633	48	100.0	356	2	Q98UK5_BRABE	Q98uk5_briachydantio
561	48	100.0	332	2	Q5B4K6_EMENTI	Q5b4k6_aspergillus	634	48	100.0	357	2	Q8B0C1_MOUSE	Q8bgc1_mus muscu
562	48	100.0	332	2	Q52KJ2_MOUSE	Q52kj2_mus muscu	635	48	100.0	357	2	Q7T2M1_BRABE	Q7t2w1_briachydantio
563	48	100.0	333	1	HXA1_RAT	Q08656_rattus norv	636	48	100.0	358	2	Q80411_IPONI	Q80411_ipomoea n1l
564	48	100.0	333	1	SPB8_ARATH	Q08x13_arabidopsis	637	48	100.0	358	2	Q76K80_ARATH	Q76k80_arabidopsis
565	48	100.0	333	2	Q8LCT0_ARATH	Q8lcv0_arabidopsis	638	48	100.0	358	2	Q10418_HCMV	Q10418_human cytom
566	48	100.0	333	2	Q4JLQ2_LACRE	Q4j1q2_lactobacill	639	48	100.0	358	2	Q69215_HCMV	Q69215_human cytom
567	48	100.0	333	2	Q4SGC1_TETNG	Q4sgc1_tetradon n	640	48	100.0	358	2	Q789F2_CHICK	Q789f2_gallus gall
568	48	100.0	334	2	Q5SG11_DICDI	Q5sg11_dicystostei	641	48	100.0	358	2	Q9DG32_XENLA	Q9dg32_xenopus lae
569	48	100.0	334	2	Q6TFR4_9BILA	Q6tfr4_ptychodera	642	48	100.0	358	2	Q4S148_TETNG	Q4s148_tetradon n
570	48	100.0	334	2	Q6TFM9_ARATH	Q6tfm9_arabidopsis	643	48	100.0	359	1	KX1_MALIZE	P24345_zea mays (m
571	48	100.0	335	1	HXA1_HUMAN	P49639_homo sapien	644	48	100.0	359	1	YOM3_CABEL	Q09556_caenorhabdi
572	48	100.0	335	2	Q9SG82_ARATH	Q9sg82_arabidopsis	645	48	100.0	359	2	Q53ZFL_MALIZE	Q53zfl_zea mays (m
573	48	100.0	335	2	Q9J889_9NUCL	Q9j889_spodoptera	646	48	100.0	359	2	Q8CF90_MOUSE	Q8cf90_mus muscu
574	48	100.0	336	2	Q4JLJ7_HELTB	Q4jlj7_hellicodacta	647	48	100.0	359	2	Q789F3_CHICK	Q789f3_gallus gall
575	48	100.0	336	2	Q4JLJ8_HELTB	Q4jlj8_hellicodacta	648	48	100.0	359	2	Q4R1R1_TETNG	Q4r1r1_tetradon n
576	48	100.0	336	2	Q9AY44_ORYSA	Q9ay44_oryza sativ	649	48	100.0	361	2	Q54MY4_DICDI	Q54my4_dicystostei
577	48	100.0	336	2	Q7XC32_ORYSA	Q7xc32_oryza sativ	650	48	100.0	361	2	Q60EU0_ORYSA	Q60eu0_oryza sativ
578	48	100.0	336	2	Q8BN18_MOUSE	Q8bn18_mus muscu	651	48	100.0	362	2	Q9ATS8_9POAL	Q9ats8_cymbopogon
579	48	100.0	336	2	Q6P4Y7_XENTR	Q6p4y7_xenopus tro	652	48	100.0	363	2	Q5A5V5_CANAL	Q5a5v5_candida alb
580	48	100.0	337	2	Q80ZAA_MOUSE	Q80zaa_mus muscu	653	48	100.0	364	2	Q6VMJ3_LUPDE	Q6vmj3_lupinus den
581	48	100.0	337	2	Q566M1_XENTR	Q566m1_xenopus tro	654	48	100.0	364	2	Q6WJ32_LUPDE	Q6wj32_lupinus den
582	48	100.0	337	2	Q6DEB7_XENLA	Q6deb7_xenopus lae	655	48	100.0	364	2	Q6YU11_ORYSA	Q6yu11_oryza sativ
583	48	100.0	338	1	IARI_ARATH	Q9me47_arabidopsis	656	48	100.0	364	2	Q6Y196_BRABE	Q6y196_briachydantio
584	48	100.0	338	2	Q80YR1_MOUSE	Q80yrt1_mus muscu	657	48	100.0	365	2	Q9AB80_CAUCR	Q9ab80_calobacter
585	48	100.0	338	2	Q5RF3E1_CHICK	Q5rf3e1_gallus gall	658	48	100.0	366	2	Q9AT80_9POAL	Q9at80_bochiriopedi
586	48	100.0	338	2	Q4RNC8_TETNG	Q4rnc8_tetradon n	659	48	100.0	366	2	Q9ATS4_9POAL	Q9ats4_capillipedi
587	48	100.0	339	2	Q5HYJ3_HUMAN	Q5hyj3_homo sapien	660	48	100.0	366	2	Q8S7W9_ORYSA	Q8s7w9_oryza sativ
588	48	100.0	339	2	Q5TTT5_ARATH	Q5ttt5_anopheles g	661	48	100.0	366	2	Q5K549_BRABE	Q5k549_briachydantio
589	48	100.0	339	2	Q81NRI_DROME	Q81nri_drosophila	662	48	100.0	366	2	Q7SZN6_BRABE	Q7szn6_briachydantio
590	48	100.0	339	2	Q5ZE66_ORYSA	Q5ze66_oryza sativ	663	48	100.0	367	1	SELPA_BRABE	Q988v1_briachydantio
591	48	100.0	339	2	Q80XP8_MOUSE	Q80xp8_mus muscu	664	48	100.0	367	2	Q7PXF8_ANOGA	Q7pxf8_anopheles g
592	48	100.0	339	2	Q98S17_XENLA	Q98s17_xenopus lae	665	48	100.0	367	2	Q6P3K0_BRABE	Q6p3k0_briachydantio
593	48	100.0	340	2	Q941Y5_ORYSA	Q941y5_oryza sativ	666	48	100.0	368	2	Q5TOY4_ANOGA	Q5toy4_anopheles g
594	48	100.0	340	2	Q7W1L1_BORPA	Q7w1l1_bordecella	667	48	100.0	368	2	Q9S7Y1_ARATH	Q9s7y1_arabidopsis
595	48	100.0	340	2	Q7WPK2_BORBR	Q7wpk2_bordecella	668	48	100.0	368	2	Q9ZLZ1_RHIME	Q9z1z1_rhizobium m
596	48	100.0	342	2	Q5AGV0_CANAL	Q5agv0_candida alb	669	48	100.0	368	2	Q4SHV5_TETNG	Q4shv5_tetradon n
597	48	100.0	342	2	Q6EN34_ORYSA	Q6en34_oryza sativ	670	48	100.0	369	1	MAF_AVIS4	P23091_avian muscu
598	48	100.0	342	2	Q76BNT1_ORYSA	Q76bnt1_oryza sativ	671	48	100.0	369	1	MAF_RAT	P54844_rattus norv
599	48	100.0	343	2	Q9DG50_XENLA	Q9dg50_xenopus lae	672	48	100.0	369	2	Q59K07_CANAL	Q59k07_candida alb
600	48	100.0	344	2	Q91BA2_NPST	Q91ba2_spodoptera	673	48	100.0	369	2	Q6DN06_SHEEP	Q6dn06_ovis aries
601	48	100.0	345	2	Q59YG2_CANAL	Q59yg2_candida alb	674	48	100.0	369	2	Q7W213_BORPA	Q7w213_bordecella
602	48	100.0	345	2	Q4ZL62_PSEBSM	Q4zl62_pseudomonas	675	48	100.0	369	2	Q7WQZ1_BORBR	Q7wqz1_bordecella
603	48	100.0	345	2	Q87TV3_PSEBSM	Q87tv3_pseudomonas	676	48	100.0	369	2	Q92171_CHICK	Q92171_gallus gall
604	48	100.0	346	2	Q4K3D2_PSEBSM	Q4k3d2_pseudomonas	677	48	100.0	370	1	MAF_MOUSE	P54843_mus muscu
605	48	100.0	346	2	Q4U1U0_XENTR	Q4u1u0_xenopus tro	678	48	100.0	370	2	Q71A33_HUMAN	Q71a33_homo sapien
606	48	100.0	346	2	Q4T9B1_TETNG	Q4t9b1_tetradon n	679	48	100.0	370	2	Q68AD2_DICDI	Q68ad2_dicystostei
607	48	100.0	348	2	Q7PT15_ANOGA	Q7pt15_anopheles g	680	48	100.0	370	2	Q9W368_DROME	Q9w368_drosophila
608	48	100.0	348	2	Q49457_ARATH	Q49457_arabidopsis	681	48	100.0	370	2	Q6H666_ORYSA	Q6h666_oryza sativ
609	48	100.0	348	2	Q6VBA4_ORYSA	Q6vba4_oryza sativ	682	48	100.0	370	2	Q5PPD0_9ALPH	Q5ppd0_suid herpes
610	48	100.0	349	2	Q92X29_RHIME	Q92x29_rhizobium m	683	48	100.0	371	2	Q9MAL7_ARATH	Q9mal7_arabidopsis
611	48	100.0	349	2	Q8YNF0_ANASP	Q8ynf0_anabaena sp	684	48	100.0	371	2	Q7VUK2_BORPE	Q7vuk2_bordecella
612	48	100.0	350	1	ROUHG_DROME	P10181_drosophila	685	48	100.0	372	2	Q5AMK8_CANAL	Q5amk8_candida alb
613	48	100.0	350	1	Q4V714_DROME	Q4v714_drosophila	686	48	100.0	372	2	Q8N7W6_HUMAN	Q8n7w6_homo sapien
614	48	100.0	351	1	CAV2_CABEL	Q18879_caenorhabdi	687	48	100.0	373	2	Q6E147_HUMAN	Q6e147_homo sapien
615	48	100.0	351	1	HREPX_PLAALO	P04929_plasmodium	688	48	100.0	373	2	Q5CDR3_CRYHO	Q5cdr3_cryptospori

669	48	100.0	373	2	081369_ARATH	081369_arabidopsis	762	48	100.0	394	2	06QB01_STRPU	06qb01_strongyloce
690	48	100.0	374	1	YMP4_CAEEL	010948_caenorhabdi	763	48	100.0	394	2	Q9XYQ3_ANOGA	Q9xyq3_anopheles
691	48	100.0	375	1	CAR2_DICDI	P34907_dictyosteli	764	48	100.0	394	2	Q7PMG4_ANOGA	Q7pmg4_anopheles
692	48	100.0	375	1	MPBP_ARATH	06dbm_arabidopsis	765	48	100.0	395	2	Q4RJS5_TETNG	Q4rjs5_tetradon
693	48	100.0	375	2	054J51_DICDI	054j51_dictyosteli	766	48	100.0	395	2	Q7SK57_AVTIS3	Q7sk57_avian sarco
694	48	100.0	375	2	054U56_DICDI	054u56_dictyosteli	767	48	100.0	396	2	Q7PYJ4_ANOGA	Q7pyj4_anopheles
695	48	100.0	376	1	TF2AA_HUMAN	P52655_h transcript	768	48	100.0	396	2	Q76KV0_PEA	Q76kv0_plum bativ
696	48	100.0	376	1	TF2AA_PONPY	05c655_p transcript	769	48	100.0	397	2	Q6MYU4_ASPFU	Q6myu4_aepexyllus
697	48	100.0	376	2	Q7QLH2_ANOGA	Q7qlh2_anopheles g	770	48	100.0	397	2	Q6S9V4_MUSDO	Q6s9v4_musca domes
698	48	100.0	376	2	Q7XA55_GNEGN	Q7xa55_gnetum gnet	771	48	100.0	397	2	Q7YLH4_ORYSA	Q7ylh4_oryza sativ
699	48	100.0	377	1	TF2AA_RAT	008949_r transcript	772	48	100.0	398	1	GAT24_ARATH	051z36_arabidopsis
700	48	100.0	377	2	Q7X9Z1_PAGES	Q7x9z1_fagopyrum e	773	48	100.0	398	2	054L08_DICDI	054lq8_dictyosteli
701	48	100.0	377	2	Q7XA00_9CARY	Q7xa00_fagopyrum h	774	48	100.0	398	2	Q70119_ANTMA	Q70119_antirrhium
702	48	100.0	377	2	Q7XA02_9CARY	Q7xa02_fagopyrum u	775	48	100.0	398	2	Q6QS35_9BETA	Q6qs35_pongine her
703	48	100.0	377	2	Q6DG75_BRARE	Q6dg75_brachydanto	776	48	100.0	399	2	052A85_MAGGR	Q5a835_magnaporthe
704	48	100.0	377	2	0804B2_BRARE	0804b2_brachydanto	777	48	100.0	399	2	Q4WU7_ASPFU	Q4wuv7_aspergillus
705	48	100.0	378	1	TF2AA_MOUSE	098pm3_m transcript	778	48	100.0	401	1	NMA1_YEAST	066178_saccharomyc
706	48	100.0	378	1	Q75GL1_ORYSA	Q75gl1_oryza sativ	779	48	100.0	401	2	0615J2_CABBR	0615j2_caenorhabdi
707	48	100.0	378	2	Q7X9Z2_9CARY	Q7x9z2_fagopyrum c	780	48	100.0	402	1	POXM_DROME	P23757_drosophila
708	48	100.0	378	2	Q7XA05_9CARY	Q7xa05_fagopyrum u	781	48	100.0	402	2	Q7PD80_ANOGA	Q7pd80_anopheles
709	48	100.0	379	1	HSBH1_SOYBN	P46608_glycine max	782	48	100.0	402	2	Q7OKT8_ANOGA	Q7okt8_anopheles
710	48	100.0	379	2	05CTA6_CRYPV	05cta6_cryptospori	783	48	100.0	402	2	Q9G0P9_DROME	Q9gqp9_drosophila
711	48	100.0	379	2	Q7X9Y8_9CARY	Q7x9y8_fagopyrum s	784	48	100.0	402	2	08MLD0_DROME	08mld0_drosophila
712	48	100.0	379	2	Q7X9Z3_9CARY	Q7x9z3_fagopyrum s	785	48	100.0	403	1	MAF_HUMAN	Q74444_homo sapien
713	48	100.0	379	2	Q7X9Z5_9CARY	Q7x9z5_fagopyrum p	786	48	100.0	403	2	Q93WJ9_ARATH	Q93wj9_arabidopsis
714	48	100.0	379	2	Q7X9Z8_9CARY	Q7x9z8_fagopyrum c	787	48	100.0	403	2	Q90Y49_AMBME	Q90y49_ambystoma m
715	48	100.0	379	2	Q7XA04_9CARY	Q7xa04_fagopyrum g	788	48	100.0	404	2	Q9M9U6_ARATH	Q9m9u6_arabidopsis
716	48	100.0	379	2	05BJV8_RAT	05bjv8_rattus norv	789	48	100.0	404	2	064875_ARATH	064875_arabidopsis
717	48	100.0	380	1	CAR2_CHARE	P24258_chlamdomon	790	48	100.0	404	2	Q8UVJ4_PETMA	Q8uvj4_petromyzon
718	48	100.0	380	2	Q7X9T7_9CARY	Q7x9t7_fagopyrum s	791	48	100.0	406	2	Q5QLP5_ORYSA	Q5qlp5_oryza sativ
719	48	100.0	380	2	Q7X9Z7_9CARY	Q7x9z7_fagopyrum s	792	48	100.0	407	2	Q4FJL4_DICDI	Q4fjl4_dictyosteli
720	48	100.0	380	2	Q7X9Z9_9CARY	Q7x9z9_fagopyrum c	793	48	100.0	407	2	Q84WQ3_ARATH	Q84wq3_arabidopsis
721	48	100.0	380	2	Q7XA03_9CARY	Q7xa03_fagopyrum c	794	48	100.0	407	2	Q9ZQA3_ARATH	Q9zqa3_arabidopsis
722	48	100.0	380	2	Q4QY62_MOUSE	Q4qy62_mus musculu	795	48	100.0	407	2	Q7V242_PROMP	Q7v242_pichlorococ
723	48	100.0	381	2	Q7X9Y9_9CARY	Q7x9y9_fagopyrum g	796	48	100.0	409	1	BAG7_YEAST	Q12128_saccharomyc
724	48	100.0	381	2	Q7XKU0_ORYSA	Q7xku0_oryza sativ	797	48	100.0	410	1	PO4FZ7_HUMAN	Q12837_homo sapien
725	48	100.0	381	2	Q5UK17_ORYSA	Q5uk17_oryza sativ	798	48	100.0	411	1	PO4FZ2_MOUSE	Q63934_mus musculu
726	48	100.0	381	2	Q9ZMD8_RHIME	Q9zmd8_rhizobium m	799	48	100.0	411	2	P78701_METAN	P78701_methazetium
727	48	100.0	382	2	Q4WMA9_ASPFU	Q4wma9_aspergillus	800	48	100.0	411	2	Q604X5_HUMAN	Q604x5_homo sapien
728	48	100.0	382	2	Q7X9Z4_9CARY	Q7x9z4_fagopyrum r	801	48	100.0	411	2	Q9SSV1_DROME	Q9ssv1_drosophila
729	48	100.0	384	2	Q6IXU1_CABBR	Q6ixu1_caenorhabdi	802	48	100.0	411	2	Q9VVM5_DROME	Q9vwm5_drosophila
730	48	100.0	384	2	Q5QLF6_ORYSA	Q5qlf6_oryza sativ	803	48	100.0	411	2	Q8CHJ4_RAT	Q8chj4_rattus norv
731	48	100.0	384	2	08Z136_PEA	08z136_plum bativ	804	48	100.0	412	2	Q91XZ7_MAGGR	Q91xz7_magnaporthe
732	48	100.0	384	2	Q6XZM1_BRARE	Q6xzm1_brachydanto	805	48	100.0	412	2	Q98U15_LAMJA	Q98u15_lampetra ja
733	48	100.0	385	1	SEPP1_RAT	P25236_rattus norv	806	48	100.0	412	2	Q4UIT8_BRARE	Q4uit8_brechydanto
734	48	100.0	385	2	Q5A5T7_CANAL	Q5a5t7_candida alb	807	48	100.0	413	2	Q8JOY8_CRYNV	Q8joy8_cryptococcu
735	48	100.0	385	2	Q17909_CAEEL	Q17909_caenorhabdi	808	48	100.0	413	2	Q8J108_CRYNV	Q8j108_cryptococcu
736	48	100.0	387	1	Q1N_AVTIS3	P36260_avian sarco	809	48	100.0	413	2	Q6GYR6_PRRYP	Q6gyr6_rypanosoma
737	48	100.0	387	2	Q7PXZ4_ANOGA	Q7pxz4_anopheles g	810	48	100.0	413	2	Q6NLK3_ARATH	Q6nlk3_arabidopsis
738	48	100.0	387	2	Q94LQ6_ORYSA	Q94lq6_oryza sativ	811	48	100.0	414	1	Q5ICW3_LAMFL	Q5icw3_lampetra fl
739	48	100.0	388	2	Q9SRJ32_DROME	Q9srj32_drosophila	812	48	100.0	414	1	TYV1_HUMAN	Q95y80_homo sapien
740	48	100.0	388	2	Q9VPA8_DROME	Q9vpa8_drosophila	813	48	100.0	414	2	TYV1_MOUSE	Q95y80_clarkia bre
741	48	100.0	388	2	Q7Y1X7_ORYSA	Q7y1x7_oryza sativ	814	48	100.0	414	2	Q6ZOB3_MOUSE	Q6zob3_mus musculu
742	48	100.0	388	2	Q8LNL6_ORYSA	Q8lnl6_oryza sativ	815	48	100.0	415	2	Q7XIX8_ORYSA	Q7xix8_oryza sativ
743	48	100.0	388	2	Q941M8_ORYSA	Q941m8_oryza sativ	816	48	100.0	419	2	Q5T2Z7_HUMAN	Q5t2z7_homo sapien
744	48	100.0	388	2	Q4S7V3_TETNG	Q4s7v3_tetradon n	817	48	100.0	419	2	Q9SY80_ORYSA	Q9sy80_oryza sativ
745	48	100.0	389	2	Q7X9I0_ARATH	Q7x9i0_arabidopsis	818	48	100.0	419	2	Q5WMS9_ORYSA	Q5wms9_oryza sativ
746	48	100.0	390	1	CBL_MLVCN	P23192_cae-nu-1 mu	819	48	100.0	419	2	Q7T2N8_BRARE	Q7t2n8_brechydanto
747	48	100.0	390	1	PC_DROME	P26017_drosophila	820	48	100.0	420	1	YBE1_SCHPO	Q42980_schizosacch
748	48	100.0	390	2	Q5ZEK4_MAGGR	Q5zek4_magnaporthe	821	48	100.0	420	2	Q5CFT6_CRYHO	Q5cft6_cryptospori
749	48	100.0	390	2	Q541F9_DROME	Q541f9_drosophila	822	48	100.0	420	2	Q9QVZ9_SMORE	Q9qvz9_mus sp. . b
750	48	100.0	390	2	Q4QB70_LEIWA	Q4qb70_leishmania	823	48	100.0	420	2	Q73862_BRARE	Q73862_brechydanto
751	48	100.0	390	2	Q661T4_XENLA	Q661t4_xenopus lae	824	48	100.0	420	2	Q568V0_BRARE	Q568v0_brechydanto
752	48	100.0	390	2	Q4V872_XENLA	Q4v872_xenopus lae	825	48	100.0	420	2	Q4SON1_TETNG	Q4son1_tetradon n
753	48	100.0	391	2	Q7SB14_NEYCR	Q7sb14_neutrospora	826	48	100.0	421	1	PO4FL1_MOUSE	P17208_mus musculu
754	48	100.0	391	2	Q9MAH8_ARATH	Q9mah8_arabidopsis	827	48	100.0	421	2	Q64FW2_MOUSE	Q64fm2_mus musculu
755	48	100.0	391	2	Q23038_ARATH	Q23038_arabidopsis	828	48	100.0	421	2	Q7BNAS_MOUSE	Q7bnas_mus musculu
756	48	100.0	392	1	ODD_DROME	P23803_drosophila	829	48	100.0	422	2	Q18452_9ASCI	Q18452_herdmania c
757	48	100.0	392	2	Q5DE72_SCHJA	Q5de72_schistosoma	830	48	100.0	422	2	Q9W4E5_DROME	Q9w4e5_drosophila
758	48	100.0	392	2	Q5CV98_CRYPV	Q5cv98_cryptospori	831	48	100.0	422	2	Q4SZ36_TETNG	Q4sz36_tetradon n
759	48	100.0	392	2	Q614Y5_CABBR	Q614y5_caenorhabdi	832	48	100.0	423	1	PO4JF1_HUMAN	Q01851_homo sapien
760	48	100.0	392	2	Q810A6_CAEEL	Q810a6_caenorhabdi	833	48	100.0	423	2	OS1JF1_MAGGR	OS1jf1_magnaporthe
761	48	100.0	394	2	Q5D114_SCHJA	Q5d114_schistosoma	834	48	100.0	423	2	O10417_HCMV	O10417_human cytom

835	48	100.0	424	2	05CJ23_CRYHO	05cJ23 cryptospori	908	48	100.0	456	2	095WD6_9ANNE	095wd6 pristina lae
836	48	100.0	424	2	04RG16_TERNG	04rg16 tetracodon n	909	48	100.0	456	2	07X637_ORYSA	07x637 oryza sativ
837	48	100.0	425	1	LE756_CAEEL	01184 caenorhabdi	910	48	100.0	456	2	08BS83_MOUSE	08bs83 mus musculu
838	48	100.0	425	1	POU1_BRARE	P31366 brachydantio	911	48	100.0	456	2	06MYT7_BRARE	06myt7 brachydantio
839	48	100.0	425	2	06OV83_CAEBR	06ov83 caenorhabdi	912	48	100.0	456	2	05MD20_BRARE	05md20 brachydantio
840	48	100.0	425	2	05CUTI_CRYPV	05cuti1 cryptospori	913	48	100.0	457	2	07SGR7_NEUCR	07sgr7 neurospora
841	48	100.0	425	2	05VWM2_ORYSA	05vwm2 oryza sativ	914	48	100.0	457	2	06P440_HUMAN	06p440 homo sapien
842	48	100.0	426	2	093ZP9_ARATH	093zpw9 arabidopsi	915	48	100.0	457	2	05JY75_HUMAN	05jy75 homo sapien
843	48	100.0	426	2	091KX1_ARATH	091kx1 arabidopsi	916	48	100.0	459	2	04ST96_TERNG	04st96 tetracodon n
844	48	100.0	427	1	CP1A_DROME	P16241 drosophila	917	48	100.0	460	2	09YL03_DROME	09yl03 drosophila
845	48	100.0	427	1	086P26_DROME	086p26 drosophila	918	48	100.0	461	2	07Q208_ANOGA	07q208 anopheles g
846	48	100.0	427	2	06VM73_LUPAL	06vm73 lupinus alb	919	48	100.0	461	2	09D709_MOUSE	09d709 mus musculu
847	48	100.0	427	2	08S3Q9_ORYSA	08s3q9 oryza sativ	920	48	100.0	461	2	091Y45_MOUSE	091y45 mus musculu
848	48	100.0	427	2	06ZJG0_ORYSA	06zjg0 oryza sativ	921	48	100.0	461	2	08VE28_MOUSE	08ve28 mus musculu
849	48	100.0	427	2	05YNG3_NOCFA	05yng3 nocardia fa	922	48	100.0	461	2	06PHC9_BRARE	06phc9 brachydantio
850	48	100.0	428	1	FOX82_MOUSE	064733 mus musculu	923	48	100.0	461	2	05MD19_BRARE	05md19 brachydantio
851	48	100.0	428	2	0811L7_PLAF7	0811l7 plasmodium	924	48	100.0	462	2	07SYH2_XENLA	07syh2 xenopus lae
852	48	100.0	428	2	05NKS7_SORBI	05nks7 sorghum bic	925	48	100.0	462	2	07ZY91_XENLA	07zy91 xenopus lae
853	48	100.0	429	2	051088_XENTR	051088 xenopus tro	926	48	100.0	463	2	054ZC9_DICDI	054zc9 dictyosteli
854	48	100.0	430	2	0624C6_CAEBR	0624c6 caenorhabdi	927	48	100.0	463	2	054Y39_DICDI	054y39 dictyosteli
855	48	100.0	431	2	081QG2_DROME	081qg2 drosophila	928	48	100.0	463	2	04ST87_TERNG	04st87 tetracodon n
856	48	100.0	431	2	09VFP2_DROME	09vfp2 drosophila	929	48	100.0	465	1	HNPF6_HUMAN	09ubc0 homo sapien
857	48	100.0	432	2	05VYV0_HUMAN	05vyv0 homo sapien	930	48	100.0	465	1	HNPF6_MOUSE	008755 mus musculu
858	48	100.0	434	2	091765_XENLA	091765 xenopus lae	931	48	100.0	465	1	HNPF6_RAT	P70512 rattus norv
859	48	100.0	434	2	07T1R4_XENTR	07t1r4 xenopus tro	932	48	100.0	465	1	0801E5_XENLA	0801e5 xenopus lae
860	48	100.0	435	2	04WU10_ASPFU	04wu10 aspergillus	933	48	100.0	466	1	ZIC3_MOUSE	062521 mus musculu
861	48	100.0	435	2	053PPE_ORYSA	053ppe oryza sativ	934	48	100.0	466	2	05CDT8_CRYHO	05cdt8 cryptospori
862	48	100.0	436	2	09YHCS_XENLA	09yhcs xenopus lae	935	48	100.0	466	2	06AVY5_ORYSA	06avy5 oryza sativ
863	48	100.0	437	1	POU12_BRARE	P56224 brachydantio	936	48	100.0	467	1	ZIC3_HUMAN	064481 homo sapien
864	48	100.0	437	2	05CXM3_CRYPV	05cxm3 cryptospori	937	48	100.0	467	2	092VX2_ARATH	092vx2 arabidopsi
865	48	100.0	437	2	060S46_CAEBR	060s46 caenorhabdi	938	48	100.0	467	2	09M117_ARATH	09m117 arabidopsi
866	48	100.0	437	2	07YWN5_CAEEL	07ywn5 caenorhabdi	939	48	100.0	467	2	09YGC6_XENLA	09ygc6 xenopus lae
867	48	100.0	437	2	06VM69_9PBAZ	06vm69 gelistera ten	940	48	100.0	469	1	ADA2C2_DIDMA	P53405 didelphis m
868	48	100.0	439	2	04IEA5_GIBZE	04iea5 gibberella	941	48	100.0	469	1	FOXGA_HUMAN	P55315 homo sapien
869	48	100.0	439	2	09NSV0_HUMAN	09nsv0 homo sapien	942	48	100.0	469	2	08H9F6_ARATH	08h9f6 arabidopsi
870	48	100.0	439	2	067U27_ORYSA	067u27 oryza sativ	943	48	100.0	470	2	05BC50_EMENT	05bc50 aspergillus
871	48	100.0	440	2	04QBP5_LEIMA	04qbp5 leishmania	944	48	100.0	470	2	0621S9_CAEEL	0621s9 caenorhabdi
872	48	100.0	441	1	08T1W3_DICDI	P46153 rattus norv	945	48	100.0	470	2	09JMA3_MOUSE	09jma3 mus musculu
873	48	100.0	441	1	POU23_BRARE	P79745 brachydantio	947	48	100.0	473	1	KNOB_PLAF7	P13817 plasmodium
874	48	100.0	443	1	POU23_BRARE	04vxa8 homo sapien	948	48	100.0	474	1	ANA_DROME	026307 drosophila
875	48	100.0	443	2	0504D2_BRARE	0504d2 brachydantio	949	48	100.0	474	2	05B4J3_EMENT	05b4j3 aspergillus
876	48	100.0	443	2	091863_FUGRU	091863 fugu rubrip	950	48	100.0	474	2	075G12_ORYSA	075g12 oryza sativ
877	48	100.0	444	1	FOXK2_HUMAN	012947 homo sapien	951	48	100.0	474	2	06DIT5_XENTR	06dit5 xenopus tro
878	48	100.0	444	1	GATNA5_MOUSE	061169 mus musculu	952	48	100.0	475	2	06BIV5_DEBHA	06biv5 debrayomyce
879	48	100.0	444	1	OSTGJ1_HUMAN	05egj1 homo sapien	953	48	100.0	475	2	Q7XQK6_ORYSA	07xqk6 oryza sativ
880	48	100.0	444	2	0657M9_ORYSA	0657m9 oryza sativ	954	48	100.0	476	2	055FD4_DICDI	055fd4 dictyosteli
881	48	100.0	444	2	07ZU22_BRARE	07zu22 brachydantio	955	48	100.0	477	1	FOXGB_HUMAN	P55315 homo sapien
882	48	100.0	444	2	06PHH6_BRARE	06phh6 brachydantio	956	48	100.0	477	2	0815Y7_ARATH	0815y7 arabidopsi
883	48	100.0	444	2	090ZS9_BRARE	090zsg9 brachydantio	957	48	100.0	477	2	09M1K5_ARATH	09m1k5 arabidopsi
884	48	100.0	444	2	04RXP7_TERNG	04rxp7 tetracodon n	958	48	100.0	479	2	05A726_CANAL	05a726 candida alb
885	48	100.0	446	2	054QY7_DICDI	054qy7 dictyosteli	959	48	100.0	479	2	05A712_CANAL	05a712 candida alb
886	48	100.0	446	2	095J45_PIG	095j45 sus scrofa	960	48	100.0	479	2	05ABT3_CANAL	05abc5 candida alb
887	48	100.0	446	2	097727_PIG	097727 sus scrofa	961	48	100.0	479	2	05AC55_CANAL	05ac55 candida alb
888	48	100.0	446	2	08UUX4_BRARE	08uux4 brachydantio	962	48	100.0	480	1	FOXGB_RAT	000939 rattus norv
889	48	100.0	446	2	055AD2_DICDI	055ad2 dictyosteli	963	48	100.0	481	1	FOXGB_MOUSE	006987 mus musculu
890	48	100.0	447	2	09FLD7_ARATH	09fld7 arabidopsi	964	48	100.0	481	2	06ZIC1_ORYSA	06zic1 oryza sativ
891	48	100.0	447	2	PO3F1_HUMAN	003052 homo sapien	965	48	100.0	481	2	08UFP7_BRARE	08ufp7 brachydantio
892	48	100.0	448	1	PO3F1_HUMAN	07saao neurospora	966	48	100.0	482	2	Q7SH12_NEUCR	07sh12 neurospora
893	48	100.0	448	1	GATP6_HUMAN	092908 homo sapien	967	48	100.0	482	2	Q4POR1_USTMA	04por1 ustilago ma
894	48	100.0	449	1	PO3F1_MOUSE	P21952 mus musculu	968	48	100.0	483	2	Q7PSP9_ANOGA	07psp9 anopheles g
895	48	100.0	449	1	08C4J8_MOUSE	08c4j8 mus musculu	969	48	100.0	483	2	05IF16_AEDAE	05if16 aedes aegypt
896	48	100.0	449	2	07Q2X7_ANOGA	07q2x7 anopheles g	970	48	100.0	483	2	053PPT_ORYSA	053ppt oryza sativ
897	48	100.0	450	2	FOXGB_CHICK	090964 gallus gall	971	48	100.0	484	1	MECP2_MOUSE	0922d6 mus musculu
898	48	100.0	451	1	PO3F1_RAT	P20267 rattus norv	972	48	100.0	484	2	06NNC9_DROME	06nnc9 drosophila
899	48	100.0	451	1	05YFAG2_HUMAN	05efag2 homo sapien	973	48	100.0	485	1	ONEC2_HUMAN	095948 homo sapien
900	48	100.0	451	2	0969P2_HUMAN	0969p2 homo sapien	974	48	100.0	486	1	MECP2_HUMAN	P51608 macaca faec
901	48	100.0	453	2	05AN14_CANAL	05an14 candida alb	975	48	100.0	486	1	MECP2_MACFA	095198 macaca faec
902	48	100.0	453	2	04XZP4_PLACH	04xzp4 plasmodium	976	48	100.0	487	2	06XBJ3_MOUSE	06xbj3 mus musculu
903	48	100.0	453	2	05OHV6_SORBI	05ohv6 sorghum bic	977	48	100.0	487	2	Q703G1_BRANA	0703g1 braselsca na
904	48	100.0	454	2	066L07_XENLA	066l07 xenopus lae	978	48	100.0	488	2	Q5SK04_CRYNE	05sk04 cryptococcu
905	48	100.0	454	2	0736Z7_ANOGA	0736z7 anolis caro	979	48	100.0	488	2	Q5K9J5_CRYNE	05k9j5 cryptococcu
906	48	100.0	456	2	054YX8_DICDI	054yx8 dictyosteli	980	48	100.0	488	2	Q4Q509_LEIMA	04q509 leishmania

```

981 48 100.0 489 2 Q66XT7_HUMAN Q66XT7_homo sapien
982 48 100.0 490 1 MOT3_YEAST P54785_saccharomyc
983 48 100.0 490 2 OSASD2_EMBL O5aed5_aspergillus
984 48 100.0 490 2 O4IGP4_GIBZE O4igp4_gliberella
985 48 100.0 490 2 OSCUA2_CRYPV O5cua2_cryptospori
986 48 100.0 491 2 O60122_EPTBU O60122_eptretus
987 48 100.0 492 1 MECP2_RAT Q00566_rattus norv
988 48 100.0 492 2 O6DKH9_HUMAN Q6dkh9_homo sapien
989 48 100.0 492 2 O9FFP2_ARATH Q9ffp2_arabidopsi
990 48 100.0 494 2 O4R113_TENG O4r113_tetradon n
991 48 100.0 495 1 PO3F3_MOUSE P31361_mus muscicu
992 48 100.0 495 2 O54QF2_DICDI O54qf2_dicystocel
993 48 100.0 496 1 BAF1_KLUMA P33293_kluyveromye
994 48 100.0 496 2 O642Y3_FUGRU O642y3_fugu rubrip
995 48 100.0 497 1 PO3F3_RAT O63262_rattus norv
996 48 100.0 497 2 O9YIB7_XENLA O9yib7_xenopus lae
997 48 100.0 498 2 O6GHH9_HUMAN O6ghh9_homo sapien
998 48 100.0 498 2 O9VWL3_DROME O9vwl3_drosophila
999 48 100.0 498 2 O9M0F8_ARATH O9m0f8_arabidopsi
1000 48 100.0 498 2 O6YSC5_ORYSA O6ysc5_oryza sativ

```

ALIGNMENTS

```

RESULT 1
LPHI_YERPE STANDARD; PRT; 15 AA.
ID LPHI_YERPE
AC Q8D079;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE His operon leader peptide (Attenuator peptide).
GN Name=hisL; OrderedlocusNames=YPO1550.1, Y2618, YP1439.1;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis.
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parthill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham T., Hamlin N., Holtroyd S., Jagsis K., Kariyeh A.V.,
RA Leather S., Moutle S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,
RT "Genome sequence of Yersinia pestis, the causative agent of plague.",
RT Nature 413:523-527(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis.
RX MEDLINE=22137863; PubMed=12142430;
DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.V., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.,
RT "Genome sequence of Yersinia pestis KIM.",
RT J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis.
RX PubMed=15368893;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.,
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
avirulent to humans.",

```

```

RL DNA Res. 11:179-197(2004).
CC -!- FUNCTION: This protein is involved in the attenuation mechanism
CC for the control of the expression of the his operon structural
CC genes (By similarity).
CC -!- SIMILARITY: Belongs to the hisL family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, AJ414149; -; NOT ANNOTATED CDS; Genomic DNA.
CC EMBL, AE013863; AA06172.1; -; Genomic DNA.
CC EMBL, AE017132; -; NOT ANNOTATED CDS; Genomic DNA.
CC InterPro: IPR012565; His leader.
CC Pfam: PF08047; His leader; 1.
CC Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis;
CC Leader peptide.
CC SEQUENCE 15 AA; 1943 MW; EE17FBF628274BD8 CRC64;
SQ

```

Query Match 100.0%; Score 48; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Gaps 0;

```

QY 1 HHHHHH 6
DB 8 HHHHHH 13

```

```

RESULT 2
LPHI_ECO57 STANDARD; PRT; 16 AA.
ID LPHI_ECO57
AC Q8X8T5;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE His operon leader peptide (Attenuator peptide).
GN Name=hisL; OrderedlocusNames=23180, EC82819;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glaesner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackert J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.",
RT Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Matsuo E., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasekawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.",
RT DNA Res. 8:11-22(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
CC -!- FUNCTION: This protein is involved in the attenuation mechanism
CC for the control of the expression of the his operon structural
CC genes (By similarity).
CC -!- SIMILARITY: Belongs to the hisL family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL, AE005174; AAG57077.1; -; Genomic_DNA.
 DR EMBL, BA000007; BAB36242.1; -; Genomic_DNA.
 DR PIR, A85827; A85827.
 DR PIR, C90981; C90981.
 DR InterPro, IPR012565; His leader.
 DR Pfam, PF08047; His leader; 1.
 KW Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis;
 KW Leader peptide.
 SQ SEQUENCE 16 AA; 2072 MW; D78A907BF6283BBA CRC64;

Query Match 100.0%; Score 48; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 9 HHHHHH 14

RESULT 3

LPHI_ECOL6 STANDARD; PRT; 16 AA.

AC P60956; P03058; (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE His operon leader peptide (Attenuator peptide).
 GN Name=hisL; OrderedLocustNames=C5496;
 OS Escherichia coli O6.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=O6.H1 / CPT073 / ATCC 700928 / UPEC;
 RX MEDLINE=2238234; PubMed=12471157; DOI=10.1073/pnas.252529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Raeko D., Buckles E.L., Lion S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

CC -!- FUNCTION: This protein is involved in the attenuation mechanism
 CC for the control of the expression of the his operon structural
 CC genes (by similarity).

CC -!- SIMILARITY: Belongs to the hisL family.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL, AE016762; AAN81000.1; -; Genomic_DNA.

DR InterPro, IPR012565; His leader.

DR Pfam, PF08047; His leader; 1.

KW Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis;
 KW Leader peptide.

SQ SEQUENCE 16 AA; 2081 MW; C8B7907BF6283BBA CRC64;

Query Match 100.0%; Score 48; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 8 HHHHHH 13

RESULT 4

LPHI_ECOL1 STANDARD; PRT; 16 AA.

AC P60955; P03058; (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE His operon leader peptide (Attenuator peptide).
 GN Name=hisL; OrderedLocustNames=b2018;

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=K12;

RX MEDLINE=79033821; PubMed=360215;

RA Dinocera P.P., Biasi F., Dilauro R., Frunzio R., Bruni C.B.;

RT "Nucleotide sequence of the attenuator region of the histidine operon
 region of Escherichia coli K-12.";

RL Proc. Natl. Acad. Sci. U.S.A. 75:4276-4280(1978).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=K12;

RX MEDLINE=82059525; PubMed=6170941;

RA Verde P., Frunzio R., di Nocera P.P., Biasi F., Bruni C.B.;

RT "Identification, nucleotide sequence and expression of the regulatory
 region of the histidine operon of Escherichia coli K-12.";

RL Nucleic Acids Res. 9:2075-2086(1981).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=K12;

RX MEDLINE=83094829; PubMed=3062174;

RA Carlomagno M.S., Chiarotelli L., Alfano P., Nappo A.G., Bruni C.B.;

RT "Structure and function of the Salmonella typhimurium and Escherichia
 coli K-12 histidine operons.";

RL J. Mol. Biol. 203:585-606(1988).

RN [4]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

CC -!- FUNCTION: This protein is involved in the attenuation mechanism
 CC for the control of the expression of the his operon structural
 CC genes.

CC -!- SIMILARITY: Belongs to the hisL family.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL, V00285; CAA23550.1; -; Genomic_DNA.

DR EMBL, V00284; CAA23548.1; -; Genomic_DNA.

DR EMBL, X13462; CAA31810.1; -; Genomic_DNA.

DR EMBL, U00096; AAC75079.1; -; Genomic_DNA.

DR PIR, A03594; LFECH.

DR ECHOBASE, EB1248; -;

DR EcoGene, EG11269; hisL.

DR InterPro, IPR012565; His leader.

DR Pfam, PF08047; His leader; 1.

KW Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis;
 KW Leader peptide.

SQ SEQUENCE 16 AA; 2081 MW; C8B7907BF6283BBA CRC64;

Query Match 100.0%; Score 48; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
Db 8 HHHHH 13

RESULT 5

LPPI_KLEPN STANDARD; PRT; 16 AA.

AC Q48439;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE His operon leader peptide (Attenuator peptide).
GN Name=hisL;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;

RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE=8413578; PubMed=6321433;

RA Rodriguez R.L., West R.W. Jr.;
RT "Histidine operon control region of Klebsiella pneumoniae: analysis with an Escherichia coli promoter-probe plasmid vector."
RL J. Bacteriol. 157:764-771(1984).

CC -!- FUNCTION: This protein is involved in the attenuation mechanism for the control of the expression of the his operon structural genes (By similarity).
CC -!- SIMILARITY: Belongs to the hisL family.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; K01997; AAA25072.1; -!- Genomic DNA.

DR InterPro; IPR012565; His_leader.

DR Pfam; PF08047; His_leader; 1.

KW Amino-acid biosynthesis; Histidine biosynthesis; leader peptide.

SQ SEQUENCE 16 AA; 2002 MW; CF29907BF6296248 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
Db 9 HHHHH 14

RESULT 6

LPPI_SALTY STANDARD; PRT; 16 AA.

AC P60957; P03058;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE His operon leader peptide (Attenuator peptide).
GN Name=hisL; OrderedLocustNames=STM2070.1;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=LT2;

RX MEDLINE=79033822; PubMed=360216;

RA Barnes W.W.;
RT "DNA sequence from the histidine operon control region: seven

RT histidine codons in a row.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:4281-4285(1978).

RN [2]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=8904829; PubMed=3062174;

RA Carlomagno W.S., Chiarotelli L., Alfano P., Nappo A.G., Bruni C.B.;

RT "Structure and function of the Salmonella typhimurium and Escherichia

RL coli K-12 histidine operons.";
RL J. Mol. Biol. 203:585-606(1988).

RN [3]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=LT2;

RA Barnes W.W., Huseon R.N., Whittier R.;

RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.

RN [4]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).

RC STRAIN=LT2 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;

RT "Complete genome sequence of Salmonella enterica serovar Typhimurium

RL LT2.";

CC -!- FUNCTION: This protein is involved in the attenuation mechanism for the control of the expression of the his operon structural

CC genes (By similarity).
CC -!- SIMILARITY: Belongs to the hisL family.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; V01371; CAA24656.1; -!- Genomic DNA.

DR EMBL; X13464; CAA31821.1; -!- Genomic DNA.

DR EMBL; J01804; AAB8613.1; -!- Genomic DNA.

DR EMBL; AE008791; -!- NOT_ANNOTATED_CDS; Genomic DNA.

DR ScyGene; SG10166; hisL.

DR InterPro; IPR012565; His_leader.

DR Pfam; PF08047; His_leader; 1.

KW Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis;

SQ SEQUENCE 16 AA; 2081 MW; C8B7907BF6283BBA CRC64;

Query Match 100.0%; Score 48; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
Db 8 HHHHH 13

RESULT 7

Q5CSK5_SCHUA PRELIMINARY; PRT; 30 AA.

AC Q5CSK5;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;

RP NUCLEOTIDE SEQUENCE.

RA Han Z.;

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY809180; AAX25069.1; -, mRNA.
 KW Hypothetical protein.
 SO SEQUENCE 30 AA; 3637 MW; FF50EE3B02EA533D CRC64;

Query Match 100.0%; Score 48; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 10 HHHHHH 15

RESULT 8
 O6UGP2_PEA PRELIMINARY; PRT; 31 AA.

AC O6UGP2;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Sacs (Fragment).
 OS Pisum sativum subsp. abyssinicum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_TaxID=198035;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Statstom J.P., Ingram P.A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY370645; AAO67403.1; -, Genomic_DNA.
 FT NON TER 31

SO SEQUENCE 31 AA; 3668 MW; B5CCC671448C064E CRC64;

Query Match 100.0%; Score 48; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 19 HHHHHH 24

RESULT 9
 O6UGP3_PEA PRELIMINARY; PRT; 31 AA.

AC O6UGP3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Sacs (Fragment).
 OS Pisum sativum subsp. elatius.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_TaxID=47742;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Statstom J.P., Ingram P.A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY370644; AAO67402.1; -, Genomic_DNA.
 FT NON TER 31

SO SEQUENCE 31 AA; 3668 MW; B5CCC671448C064E CRC64;

Query Match 100.0%; Score 48; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 19 HHHHHH 24

RESULT 10
 O6UGP5_PEA PRELIMINARY; PRT; 31 AA.

AC O6UGP5;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Sacs (Fragment).
 OS Pisum sativum var. pumilio.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_TaxID=51234;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Statstom J.P., Ingram P.A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY370642; AAO67400.1; -, Genomic_DNA.
 FT NON TER 31

SO SEQUENCE 31 AA; 3668 MW; B5CCC671448C064E CRC64;

Query Match 100.0%; Score 48; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 19 HHHHHH 24

RESULT 11
 O6UGP7_PEA PRELIMINARY; PRT; 31 AA.

AC O6UGP7;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Sacs (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_TaxID=3888;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Statstom J.P., Ingram P.A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY370640; AAO67398.1; -, Genomic_DNA.
 FT NON TER 31

SO SEQUENCE 31 AA; 3668 MW; B5CCC671448C064E CRC64;

Query Match 100.0%; Score 48; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 19 HHHHHH 24

RESULT 12
 Q5SG0_MOUSE PRELIMINARY; PRT; 31 AA.

AC Q5SG0;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)

DE Heart and neural crest derivatives expressed transcript 1
 (Fragment).
 GN Name=Hand1; ORFNames=RP23-268K22.4-002;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Matthews L.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL732587; CAI24810.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 31 AA; 3636 MW; 66C64537E1C5FE8B CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
   |||||
Db 9 HHHHH 14

RESULT 13
Q4YAH2_PLABE PRELIMINARY; PRT; 34 AA.
AC Q4YAH2_
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB401314.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Omond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jance C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01007077; CAI05235.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
FT NON_TER
SQ SEQUENCE 34 AA; 4155 MW; BE4AE59E7ED365C4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
   |||||
Db 1 HHHHH 6

RESULT 14
Q65825_9BACU PRELIMINARY; PRT; 44 AA.
AC Q65825_
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE MCS protein precursor.
GN Name=MCS;
OS unidentified baculovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OX NCBI_TaxID=10469;

```

```

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96032347; PubMed=7557433; DOI=10.1016/0378-1119(95)00360-1;
RA Kuehn S., Zifel P.F.;
RT "The baculovirus expression vector pBSV-8His directs secretion of
RT histidine-tagged proteins."
RL Gene 162:225-229(1995).
DR EMBL; X87245; CAA60687.1; -; Genomic_DNA.
KW Signal.
FT SIGNAL
SQ SEQUENCE 44 AA; 4961 MW; E042D55613947925 CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
   |||||
Db 34 HHHHH 39

RESULT 15
Q5ISM1_MACFA PRELIMINARY; PRT; 46 AA.
ID Q5ISM1_
AC Q5ISM1_
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Distal-less homeobox 2 protein (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15620360; DOI=10.1016/j.cell.2004.11.040;
RA Dorus S., Vallender E.J., Evans P.D., Anderson J.R., Gilbert S.L.,
RA Malwald M., Wyckoff E.J., Malcom C.M., Lahn B.T.;
RT "Accelerated evolution of nervous system genes in the origin of Homo
RT sapiens."
RL Cell 119:1027-1040(2004).
DR EMBL; AY650359; AA67391.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
KW Nuclear protein.
FT NON_TER
FT NON_TER
SQ SEQUENCE 46 AA; 5081 MW; AF905B0A2829EBCB CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
   |||||
Db 40 HHHHH 45

RESULT 16
Q8SASO_PINSY PRELIMINARY; PRT; 48 AA.
ID Q8SASO_
AC Q8SASO_
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative N-terminal acetyltransferase (Fragment).
OS Pinus sylvestris (Scots pine).
OC Fungi; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxID=3349;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21660210; PubMed=11801746;

```

```

RA Dvornyk V., Sirvio A., Mikkonen M., Savolainen O.;
RT "Low nucleotide diversity at the pall locus in the widely distributed
RT Pinus sylvestris.";
RL Mol. Biol. Evol. 19:179-188(2002).
DR EMBL; AF359124; AAL74392.1; -; Genomic_DNA.
KW GO; GO:0016740; F:transferase activity; IEA.
FT NON TER
SQ SEQUENCE 48 AA; 5247 MW; FD0FD03DED4DFDDE CRC64;

Query Match 100.0%; Score 48; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 16 HHHHHH 21

RESULT 17
Q8SAS1_PINSY PRELIMINARY; PRT; 48 AA.
AC Q8SAS1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative N-terminal acetyltransferase (Fragment).
OS Pinus sylvestris (Scots pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxId=33349;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2160210; PubMed=11801746;
RA Dvornyk V., Sirvio A., Mikkonen M., Savolainen O.;
RT "Low nucleotide diversity at the pall locus in the widely distributed
RT Pinus sylvestris.";
RL Mol. Biol. Evol. 19:179-188(2002).
DR EMBL; AF359123; AAL74391.1; -; Genomic_DNA.
KW GO; GO:0016740; F:transferase activity; IEA.
FT NON TER
SQ SEQUENCE 48 AA; 5302 MW; 6A91AE3DED4DFDDB CRC64;

Query Match 100.0%; Score 48; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 16 HHHHHH 21

RESULT 18
Q5CJ22_SCHUA PRELIMINARY; PRT; 53 AA.
AC Q5CJ22;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DE 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeididae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxId=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY810244; AAX26133.1; -; mRNA.
KW InterPro; IPR012287; Homeodomain-rel.
SQ SEQUENCE 53 AA; 6363 MW; 388D373DBF1DC268 CRC64;

```

```

Query Match 100.0%; Score 48; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 13 HHHHHH 18

RESULT 19
Q55244_92ZZZ PRELIMINARY; PRT; 53 AA.
AC Q55244;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Histidine hexamer-multiple cloning site-histidine decamer.
OS Name=his6-mcs-his10;
OS plasmid pETHIS-1.
OC other sequences; plasmids.
OX NCBI_TaxId=64374;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99392473; PubMed=10463177;
RA Schaller A., Kuhn R., Kuhnert P., Nicolet J., Anderson T.J.,
RA MacInnes J.I., Segers R.P., Frey J.;
RT "Characterization of aprIVA, a new RTX determinant of Actinobacillus
RT pleuropneumoniae.";
RL Microbiology 145:2105-2116(1999).
DR EMBL; AF012911; AAB97883.1; -; Genomic_DNA.
KW plasmid
SQ SEQUENCE 53 AA; 5780 MW; BDAC93CC66B9CFF CRC64;

Query Match 100.0%; Score 48; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 5 HHHHHH 10

RESULT 20
Q4WHB8_ASPFU PRELIMINARY; PRT; 54 AA.
AC Q4WHB8;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
OS ORFNames=Atu2g05660;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxId=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nieman W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman N., Fedorova N., Fedorova N., Feldlyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulikarni R.,
RA Kumagai T., Lafont A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majors W.H., May G.S., Miller B.L., Mohammad Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penalva I.A., Pettea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,

```

```

RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Roming C.M., Ruter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Varquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Frazer C., Galagan J.E., Aebi K.,
RA Machida M., Hall N., Barrett B., Denning D.W.,
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus."
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF0100008; EAL87657.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 54 AA; 6561 MW; B65FC626A6EC9C47 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 30 HHHHHH 35

RESULT 21
OGIH19 DROME PRELIMINARY; PRT; 58 AA.
ID OG1H19
AC OG1H19
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE HDCC02522.
GN ORFNames=HDC02522;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:14709175; DOI=10.1186/gb-2003-5-1-r3;
RA Hild M., Beckmann B., Haas S.A., Koch B., Solovjev V., Bueold C.,
RA Fellenberg K., Boultos M., Vingron M., Sauer F., Hohnsbeil J.D.,
RA Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome."
RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
CC -! MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK003427; DAA03626.1; -; Genomic DNA.
SQ SEQUENCE 58 AA; 6523 MW; B6F483484C102231 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 48 HHHHHH 53

RESULT 22
HPN HELPJ STANDARD; PRT; 59 AA.
ID HPN HELPJ
AC P0A0V7; Q48251;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Histidine-rich, metal binding polypeptide.
GN Name=hpj; OrderedLocNames=HPJ320;
OS Helicobacter pylori J99 (Campylobacter J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

```

```

OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
CC -! FUNCTION: Strongly binds nickel and zinc. Binds other metals less
CC strongly: cobalt > copper > cadmium > manganese. May act to
CC increase, or at least to preserve, urease activity. Exact function
CC is still unknown (By similarity).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE001555; AAD06898.1; -; Genomic_DNA.
DR PIR; C64698; C64698.
DR HSSP; P13231; IHCE.
KW Complete proteome; Metal-binding; Nickel; Repeat; Zinc.
FT INIT MET 0 0 By similarity.
FT REPEAT 37 41 1.
FT REPEAT 50 54 2.
FT REGION 37 54 2 X 5 AA repeats of E-E-G-C-C.
FT COMPIAS 10 23 Poly-His.
FT COMPIAS 27 32 Poly-His.
SQ SEQUENCE 59 AA; 6946 MW; C3AE83F602EC973C CRC64;

Query Match 100.0%; Score 48; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 10 HHHHHH 15

RESULT 23
HPN HELPJ STANDARD; PRT; 59 AA.
ID HPN HELPJ
AC P0A0V6; Q48251;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Histidine-rich, metal binding polypeptide.
GN Name=hpj; OrderedLocNames=HPJ427;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-18 AND 47-59.
RC STRAIN=LEU.
RX MEDLINE=95310028; PubMed=7790085;
RA Gilbert J.V., Ramakrishna J., Sunderman F.W. Jr., Wright A.,
RA Platt A.G.;
RT "Protein Hpj: cloning and characterization of a histidine-rich metal-
RT binding polypeptide in Helicobacter pylori and Helicobacter
RT mucelae."
RL Infect. Immun. 63:2682-2688(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=26695 / ATCC 700392;
RC MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

```

```

RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khaila H.G.,
RA Glodok A., McInerney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Wathen L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
CC -1- FUNCTION: Strongly binds nickel and zinc. Binds other metals less
CC strongly: cobalt > copper > cadmium > manganese. May act to
CC increase, or at least to preserve, urease activity. Exact function
CC is still unknown.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; U26361; AAA85859.1; -; Genomic_DNA.
CC EMBL; AE000643; AAD08471.1; -; Genomic_DNA.
CC PIR; C64698; C64698.
CC HSSP; P13231; IHCE.
CC TIGR; HP1427; -.
DR Complete proteome; Direct protein sequencing; Metal-binding; Nickel;
KM Repeat; Zinc.
KM INIT MET 0
FT REPEAT 37 41 1.
FT REPEAT 50 54 2.
FT REGION 37 54 2 x 5 AA repeats of E-E-G-C-C.
FT COMBINS 10 23 Poly-His.
FT COMBINS 27 32 Poly-His.
SQ SEQUENCE 59 AA; 6946 MW; C3AE33F602EC973C CRC64;

Query Match 100.0%; Score 48; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 10 HHHHHH 15

RESULT 24
Q40049 HORVU PRELIMINARY; PRT; 64 AA.
ID Q40049 HORVU PRELIMINARY; PRT; 64 AA.
AC Q40049;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE ES1A protein.
GN Name=ES1A;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=95367651; PubMed=7640362;
RA Speulman B., Salami F.;
RT "GA3-regulated cDNAs from Hordeum vulgare leaves."
RL Plant Mol. Biol. 28:915-926(1995).
DR EMBL; X78884; CAA55483.1; -; mRNA.
DR PIR; SS7787; SS7787
SQ SEQUENCE 64 AA; 7155 MW; 6DECBEB843616138 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 25 HHHHHH 30

RESULT 25
Q61JH9 DROME PRELIMINARY; PRT; 66 AA.
ID Q61JH9 DROME PRELIMINARY; PRT; 66 AA.
AC Q61JH9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE HDCL4879.
GN ORFNames=HDCL4879;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
RA Hild M., Beckmann B., Haas S.A., Solovjev V., Busold C.,
RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohlseil J.D.,
RA Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome."
RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK007737; DAA04242.1; -; Genomic DNA.
SQ SEQUENCE 66 AA; 7988 MW; A68D75FCB2DB4BC CRC64;

Query Match 100.0%; Score 48; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 14 HHHHHH 19

RESULT 26
Q6R2V8 TRIPE PRELIMINARY; PRT; 69 AA.
ID Q6R2V8 TRIPE PRELIMINARY; PRT; 69 AA.
AC Q6R2V8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE HEX1 (Fragment).
GN Name=hex1;
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocremycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VT-D-79125;
RC Curach N.C., Te'o V.S.J., Gibbs M.D., Bergquist P.L.,
RA Nevalainen H.K.M.;
RT "Isolation, characterization and expression of the hex1 gene from
RT Trichoderma reesei."
RL Gene 0:0-01(2004).
DR EMBL; AY517641; AAS07013.1; -; mRNA.
FT NON TER 69
SQ SEQUENCE 69 AA; 8197 MW; 006B697EFC73570D CRC64;

Query Match 100.0%; Score 48; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 HHHHHH 6
Ox      |||||
Db      27 HHHHHH 32

RESULT 27
ID      041010 GIBZE PRELIMINARY; PRT; 69 AA.
O41010 GIBZE PRELIMINARY; PRT; 69 AA.
AC      041010;
DT      13-SEP-2005 (TREMBLrel. 31, Created)
DT      13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT      13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE      Hypothetical protein.
GN      ORFNames=FG00498.1;
OS      Glibberella zeae PH-1.
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC      Hypocryomycetidae; Hypocreales; Nectriaceae; Glibberella.
OX      NCBI_TaxID=229533;
RN      (1)
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=PH-1;
RA      Birren B., Nusbbaum C., Abouelleil A., Allen N., Anderson S.,
RA      Archchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA      Bouhagiel B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA      Choepel Y., Collymore A., Cook A., Cooke P., Cornu B., Deatrellano K.,
RA      Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA      Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA      Gardlyn S., Gierre S., Graham L., Grand-Pierre N., Hafez I.,
RA      Hagopian D., Hages B., Hall J., Horton L., Hulme W., Iller I.,
RA      Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA      Kells C., Landers T., Levine R., Lindblad-Toh K., Liu J., Lui A.,
RA      Ma L.-C., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA      Matthews C., Mauceli E., McCarthy M., Meldrum J., Meneus L.,
RA      Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA      Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA      Oliver J., Peterson K., Phukhang P., Picire N., Purcell S.,
RA      Rachupka A., Ramsamy U., Raymond C., Retta R., Rice C., Rogov P.,
RA      Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
RA      Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA      Talama J., Tefaye S., Theodore J., Topham K., Travers M.,
RA      Vassiliev H., Venkataranan V.S., Viel R., Vo A., Wang S., Wilson B.,
RA      Wu X., Wyman D., Young G., Zaitoun J., Zembek L., Zimmer A., Zody M.,
RA      Lander E.;
RT      "Fusarium graminearum genome sequence."
RL      Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
DR      EMBL; AACM0100020; EAA68730.1; -; Genomic_DNA.
KW      Hypothetical protein.
SQ      SEQUENCE 69 AA; 8441 MW; 60C3558458EDEF22 CRC64;

Query Match      100.0%; Score 48; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HHHHHH 6
Ox      |||||
Db      27 HHHHHH 32

RESULT 28
O9PT65 XENLA PRELIMINARY; PRT; 69 AA.
ID      09PT65;
AC      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE      Homeodomain transcription factor (Fragment).
CN      Name=Pltx2A;
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

```

```

OC      Xenopodinae; Xenopus; Xenopus.
OX      NCBI_TaxID=8335;
RN      (1)
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=20054091; PubMed=10585561; DOI=10.1016/S0925-4773(99)00227-0;
RA      Schweickert A., Campione M., Steinbeisser H., Blum M.;
RT      "Ptx2 isoforms: involvement of Ptx2c but not Ptx2a or Ptx2b in
RT      vertebrate left-right asymmetry.";
RL      Mech. Dev. 90:41-51(2000).
DR      EMBL; AJ243596; CAB5515.1; -; mRNA.
KW      GO: 0005634; C:nucleus; IEA.
FT      Nuclear protein.
FT      NON_TER
SQ      SEQUENCE 69 AA; 7576 MW; 19C21A42C7B30847 CRC64;

Query Match      100.0%; Score 48; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HHHHHH 6
Ox      |||||
Db      24 HHHHHH 29

RESULT 29
ID      054KT2 DICDI PRELIMINARY; PRT; 72 AA.
O54KT2 DICDI PRELIMINARY; PRT; 72 AA.
AC      054KT2;
DT      13-SEP-2005 (TREMBLrel. 31, Created)
DT      13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT      13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE      Hypothetical protein.
GN      ORFNames=DDB0218896;
OS      Dictyostelium discoideum (Slime mold).
OC      Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX      NCBI_TaxID=44689;
RN      (1)
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=XX4;
RA      Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA      Sugang R., Barriman M., Song J., Olsen R., Szafarski K., Xu Q.,
RA      Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA      Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA      Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA      Kerhroux A., Nie X., Hall N., Anjard C., Hemphill L., Basson N.,
RA      Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA      Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA      Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
RA      Hauser H., James K., Quilez M., Mohan M.B., Saito T., Buchrieser C.,
RA      Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA      Louiseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA      Urubilahara H., Hernandez J., Rabbittowltch E., Steffen D., Sanders M.,
RA      Ma J., Kohara Y., Sharp S., Simmonds M., Spegler S., Tivey A.,
RA      Sugano S., White B., Walker D., Woodward G., Rosenthal A., Cox E.C.,
RA      Shaulsky G., Schleicher M., Weinrock G., Rosenthal A., Cox E.C.,
RA      Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA      Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT      "The genome of the social amoeba Dictyostelium discoideum.";
RL      Nature 0:0-0(2005).
CC      -!- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
DR      EMBL; AAF10100148; EAL63870.1; -; Genomic_DNA.
KW      Hypothetical protein.
SQ      SEQUENCE 72 AA; 8561 MW; E495A55F52AB37A CRC64;

Query Match      100.0%; Score 48; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HHHHHH 6
Ox      |||||
Db      18 HHHHHH 23

```

```

RESULT 30
Q8T1A1_DICDI PRELIMINARY; PRT; 72 AA.
AC Q8T1A1;
DT 01-JUN-2002 (TRMBLrel. 21, Created)
DT 01-JUN-2002 (TRMBLrel. 21, Last sequence update)
DT 10-MAY-2005 (TRMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DDB0167568;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_Taxid=44689;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafrański K., Pachbat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafrański K., Pachbat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachbat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Bertrman M., Song J., Olsen R., Szafrański K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Baeson N.,
RA Farbhrou P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Salto T., Buchrieser C.,
RA Wardeper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louisgeed H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma U., Kohara Y., Sharp S., Simmonds S., Spiegler S., Tiley A.,
RA Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis M.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2003).
DR EMBL; AC116956; AAM08755.1; -; Genomic_DNA.
DR EMBL; AAF10100027; EAL69989.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ
SEQUENCE 72 AA; 8867 MW; 27CDD6A105612FDDCA CRC64;

Query Match 100.0%; Score 48; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 64 HHHHHH 69

```

```

DE Histidine and glutamine-rich protein.
GN OrderedlocusNames=HP1432;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_Taxid=210;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalaf H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weldman J.F., Fujii C., Bowman C.,
RA Wathey L., Wallin E., Hayes W.S., Borodovsky M., Karpi P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000643; AAD08472.1; -; Genomic_DNA.
DR PIR; H64698; H64698.
DR TIGR; HP1432; -.
KW Complete proteome.
SQ
SEQUENCE 72 AA; 8779 MW; 1663F1CFCDBA760D CRC64;

```

```

Query Match 100.0%; Score 48; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 16 HHHHHH 21

RESULT 32
Q8T3D9_CAEEL PRELIMINARY; PRT; 75 AA.
AC Q8T3D9;
DT 01-JUN-2002 (TRMBLrel. 21, Created)
DT 01-JUN-2002 (TRMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE Hypothetical protein F53B6.9.
GN ORFNames=F53B6.9;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG "The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81086; CAD30440.1; -; Genomic_DNA.
DR Ensembl; F53B6.9; Caenorhabditis elegans.
DR Wormbase; WBGene0009964; F53B6.9.
DR WormPep; F53B6.9; CE30539.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 75 AA; 8785 MW; 987285B255505FAC CRC64;

```

```

Query Match 100.0%; Score 48; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 34 HHHHHH 39

```

RESULT 33
 O9VLH4 DROME PRELIMINARY; PRT; 76 AA.
 AC O9VLH4_4
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE CG15867-PA.
 GN Name=CG15867; ORFNames=CG15867;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 [1]
 NP NUCLEOTIDE SEQUENCE.
 RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazet J.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burdya K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos P., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hovstett D., Houston K.A., Howland T.J., Wei W.-H., Ibegman C.,
 RA Jajaeli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laake P., Lei Y., Levitsky A.A., Li J.H., Liang Y., Lin X.,
 RA Liu X., Matel J.B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Moadarry C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitak R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of Drosophila melanogaster.";
 Science 287:2185-2195(2000).
 [2]
 NP NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams W., Champagne M., Dugan S.P., Fries E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodegryn E.J.,
 RA Svitak R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RA "Finishing a whole-genome shotgun: release 3 of the Drosophila
 melanogaster euchromatic genome sequence.";
 Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [3]
 NP NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svitak R.,
 RA Patel S., Fries E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celinker S.E.,
 RT "The transposable elements of the Drosophila melanogaster euchromatic:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart M.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celinker S., Carlson J., Wan K., Pfeiffer B., Fries E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svitak R., Smith E.,
 RA Yu C., Rubin G.,
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [6]
 NP NUCLEOTIDE SEQUENCE.
 RP Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AE003622; AA52716.1; -; Genomic DNA.
 DR Ensembl; CG15867; Drosophila melanogaster.
 DR Flybase; FBgn0040961; CG15867.
 SQ SEQUENCE 76 AA; 8473 MW; 1197B816AD64A15F CRC64;
 Qy Best Local Similarity 100.0%; Score 48; DB 2; Length 76;
 Db Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 HHHHHH 6
 13 HHHHHH 18
 RESULT 34
 Q02690 CAEBL PRELIMINARY; PRT; 77 AA.
 AC Q02690;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein F53A9.1.
 GN ORFNames=F53A9.1;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Felodierinae; Caenorhabditis.
 OC NCBI_TaxId=6239;
 [1]
 NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 283:2012-2018(1998).
 CC -I- INTERACTION:
 CC Q8MM07:cm-1, NDExp-1; InAct-EBI-312591, EBI-312477;
 CC EMBL; U23523; AAC46556.1; -; Genom1C_DNA.
 DR PIR; T16436; T16436.
 DR InAct; Q02690; -;
 DR Ensembl; F53A9.1; Caenorhabditis elegans.
 DR WormBase; WBGene00018724; F53A9.1.
 DR WormPeP; F53A9.1; C802760.
 DR InterPro; IPR006025; Pept_M_Zn_BS.

DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 77 AA; 8577 MW; 23A5D23442541D64 CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 46 HHHHHH 51

RESULT 35
 09ZJ18_HELPJ PRELIMINARY; PRT; 77 AA.
 ID 09ZJ18_HELPJ PRELIMINARY;
 AC 09ZJ18;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Putative histidine and glutamine-rich metal-binding protein.
 GN OrderedLocustNamees=JH1321;
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 CX NCBI_TaxId=85963;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonghe B.L., Carmel G.,
 RA Tumlin P.J., Carnso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.U.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).
 DR EMBL; AE001555; AAD06903.1; -; Genomic_DNA.
 DR PIR; D71821; D71821.
 KW Complete proteome.
 SQ SEQUENCE 77 AA; 9409 MW; F259778DBDB3985 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 21 HHHHHH 26

RESULT 36
 0613L0_CABR PRELIMINARY; PRT; 80 AA.
 ID 0613L0_CABR PRELIMINARY;
 AC 0613L0;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG16338.
 GN Name=CBG16338;
 OS Caenorhabditis briggsae.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodertinae; Caenorhabditis.
 CX NCBI_TaxId=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 KW Hypothetical protein.

SQ SEQUENCE 80 AA; 8906 MW; 1FF84C346C128F99 CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 74 HHHHHH 79

RESULT 37
 07JUP3_CABR PRELIMINARY; PRT; 80 AA.
 ID 07JUP3_CABR PRELIMINARY;
 AC 07JUP3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Insulin related protein 20.
 GN Name=ins-20; ORFName=ZK84.7;
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodertinae; Caenorhabditis.
 CX NCBI_TaxId=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Br1etol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RT "The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; U23181; AAR12989.1; -; Genomic DNA.
 DR Ensembl; ZK84.7; Caenorhabditis elegans.
 DR Wormbase; WBGene00002103; ZK84.7.
 DR WormPep; ZK84.7; CE36082.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0005179; P:hormone activity; IEA.
 DR GO; GO:0007582; P:physiological process; IEA.
 DR InterPro; IPR003235; Nmrde_ins_beta.
 DR ProDom; PD012623; Nmrde_ins_beta; 1.
 KW Complete proteome.
 SQ SEQUENCE 80 AA; 9357 MW; AB17117D39923D30 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 25 HHHHHH 30

RESULT 38
 061D00_CABR PRELIMINARY; PRT; 82 AA.
 ID 061D00_CABR PRELIMINARY;
 AC 061D00;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG12395.
 GN Name=CBG12395;
 OS Caenorhabditis briggsae.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodertinae; Caenorhabditis.
 CX NCBI_TaxId=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; CAAC01000060; CAE66997.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 82 AA; 9659 MW; 4039B513C6552F31 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 35 HHHHHH 40

RESULT 39
 020689 CAEEL
 ID 020689 CAEEL PRELIMINARY; PRT; 83 AA.
 AC 020689
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein F53A9.2.
 GN ORFNames=F53A9.2;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodertinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Br1stol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology."
 RL Science 282:2012-2018 (1998).
 CC -1- INTERACTION:
 CC Q8MM07:crn-1; NDEXP-1; INFACT-EB1-312596; EB1-312477;
 CC EMBL; U23523; AAC46557.1; -; Genomic_DNA.
 DR INACT; Q20689; -;
 DR PIR; T16435; T16435.
 DR INACT; Q20689; -;
 DR Ensembl; F53A9.2; Caenorhabditis elegans.
 DR WormBase; MBGene0018725; F53A9.2.
 DR WormPeP; F53A9.2; CE02762.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 83 AA; 9300 MW; DFF31DFB5C81F18 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 45 HHHHHH 50

RESULT 40
 0615X5 CAEBR
 ID 0615X5 CAEBR PRELIMINARY; PRT; 84 AA.
 AC 0615X5
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG15407.
 GN Name=CBG15407;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodertinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAC01000072; CAE69311.1; -; Genomic_DNA.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 84 AA; 9397 MW; 12C5B95F7AA516F CRC64;

Query Match 100.0%; Score 48; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 5.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 46 HHHHHH 51

RESULT 41
 058W23 ORENT
 ID 058W23 ORENT PRELIMINARY; PRT; 85 AA.
 AC 058W23
 DT 10-MAY-2005 (TReMBLrel. 30, Created)
 DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
 DE Hox protein (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphae; Acanthopterygii; Percomorphae; Perciformes; Labroidae;
 CC Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapiaini;
 OC Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B3b;
 RX PubMed=15716008; DOI=10.1016/j.gene.2004.10.027;
 RA Santini S., Bernardi G.;
 RT "Organization and base composition of tilapia Hox genes: implications
 RT for the evolution of Hox clusters in fish."
 RL Gene 346:51-61 (2005).
 DR EMBL; AY57333; AAY97676.2; -; Genomic_DNA.
 DR InterPro; IPR001827; Antennapedia.
 DR PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN_1.
 FT NON TER 85
 FT 85
 SQ SEQUENCE 85 AA; 9841 MW; 7E645627269165F8 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 14 HHHHHH 19

RESULT 42
 05TRG3 ANOGA
 ID 05TRG3 ANOGA PRELIMINARY; PRT; 86 AA.
 AC 05TRG3
 DT 01-FEB-2005 (TReMBLrel. 29, Created)
 DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
 DE ENSANGP0000029435.
 GN ORFNames=ENSANGG0000023751;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;

RG The Anopheles gambiae Sequence Committee;
RA "Anopheles gambiae re-annotation."
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008960; EAL39901.1; -; Genomic DNA.
SQ SEQUENCE 86 AA; 9902 MW; 7CFA192D4C8940FE CRC64;

Query Match 100.0%; Score 48; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 30 HHHHHH 35

RESULT 43
ID 061311 CAEBR PRELIMINARY; PRT; 87 AA.
AC 061311
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein CBG16337.
GN Name=CBG16337;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditiidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC01000076; CAB69948.1; -; Genomic DNA.
KM Hypothetical protein.
SQ SEQUENCE 87 AA; 9316 MW; F1B900A2DDB08BC4 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 52 HHHHHH 57

RESULT 44
ID 061HC6 DROME PRELIMINARY; PRT; 87 AA.
AC 061HC6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE HDC02760.
GN ORFNames=HDC02760;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Megaloptera; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;

RA Hild M., Beckmann B., Haas S.A., Koch B., Solovyev V., Busold C.,
RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hobeisel J.D.,
RA Piro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome."
RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK003490; DAA03689.1; -; Genomic DNA.
SQ SEQUENCE 87 AA; 9474 MW; 6F2616FFB03E5E7 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 23 HHHHHH 28

RESULT 45
ID 0861J5 DICDI PRELIMINARY; PRT; 89 AA.
AC 0861J5;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Similar to F22H10.2.p (Hypothetical protein).
GN ORFNames=DD80168879;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szifranski K., Pachebat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."
RT Nature 418:79-85(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugeng R., Berriman M., Song J., Olsen R., Szifranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies G., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerkorou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Fathrocher P., Desany B., Just E., Morio T., Rest R., Churcher C.,
RA Cooper J., Haydock S., van Drieseche N., Cronin A., Goodhead I.,
RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Landay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louisgeed H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrett B., Kuypa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0(2005).
DR EMBL; AC117176; AA052096.1; -; Genomic DNA.
DR EMBL; AAF10100022; EAL70996.1; -; Genomic DNA.
KM Hypothetical protein.

SQ SEQUENCE 89 AA; 10155 MW; DF4C1349B9B8E82C CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 6 HHHHHH 11

RESULT 46
 Q6EPJ7_ORYSA
 ID Q6EPJ7_ORYSA PRELIMINARY; PRT; 89 AA.

AC Q6EPJ7;
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein OSUNBa003K18.14;
 GN Name=OSUNBa003K18.14;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005875; BAD29423.1; -; Genomic_DNA.
 DR Gramene; Q6EPJ7; -;
 KM Hypothetical protein.
 SQ SEQUENCE 89 AA; 10274 MW; A6C59326FB2BD786 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 68 HHHHHH 73

RESULT 47
 Q698K8_AGKHB
 ID Q698K8_AGKHB PRELIMINARY; PRT; 89 AA.

AC Q698K8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Adinbitor (Fragment).
 OS Agdistrodon halys brevicaudus (Korean slamosa snake) (Gloydus halys brevicaudus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OC NCBI_TaxID=259325;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Venom gland;
 RA Wang J.H., Wu Y., Ren F., Zhao B.C.;
 RT "Cloning and characterization of adinbitor: a novel disintegrin from a snake venom."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY551929; AAT76292.1; -, mRNA.

DR GO; GO:0005515; F:protein binding; IEA.

DR InterPro; IPR001762; Disintegrin; IEA.

DR Pfam; PF00200; Disintegrin; 1.

DR PRINTS; PR00289; Disintegrin; 1.

DR ProDom; PD000664; Disintegrin; 1.

DR SMART; SM00050; DISIN; 1.

DR PROSITE; PS00427; DISINTEGRIN_1; 1.

DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 KW Cell adhesion.
 SQ SEQUENCE 89 AA; 9645 MW; 40BD95DCE2D7A313 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 84 HHHHHH 89

RESULT 48
 OS24U9_ORYSA
 ID OS24U9_ORYSA PRELIMINARY; PRT; 91 AA.

AC OS24U9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein P0545E05.30.
 GN Name=P0545E05.30;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005931; BAD54668.1; -, Genomic_DNA.
 KM Hypothetical protein.
 SQ SEQUENCE 91 AA; 10464 MW; E84483B6567E5342 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 15 HHHHHH 20

RESULT 49
 Q18410_CAEEL
 ID Q18410_CAEEL PRELIMINARY; PRT; 92 AA.

AC Q18410;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein C33H5.13.

GN ORFNames=C33H5.13;

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OC NCBI_TaxID=6239;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Bristol N2;

RX MEDLINE=99069613; PubMed=9851916;

RG "The C. elegans sequencing consortium";

RT Investigating biology.";

RL Science 282:2012-2018 (1998).

DR EMBL; U41007; AAA82273.1; -, Genomic_DNA.

DR PIR; T34146; T34146.

DR Ensembl; C33H5.13; Caenorhabditis elegans.

DR WormBase; WBGene0016379; C33H5.13.

DR WormPep; C33H5.13; CE04156.

KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 92 AA; 9969 MW; C91B655BA701A06 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 58 HHHHHH 63

RESULT 50

0861J4 DICDI
 ID 0861J4_DICDI PRELIMINARY; PRT; 93 AA.

AC 0861J4; 01-JUN-2003 (TRENBLREL. 24, Created)
 DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Hypothetical protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
 RA Gloeckner G., Richter V., Szafrański K., Pachbat J.A.,
 RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
 RA Abriil J.F., Guigo R., Kumpf K., Tunggal B., Cox B., Quail M.A.,
 RA Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
 RL Nature 418:79-85(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;
 RA Baumgart C.;
 RU Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC117176; A052097.1; -; Genomic_DNA.

KW Hypothetical protein.
 SQ SEQUENCE 93 AA; 10589 MW; 1A860E9A266A7637 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 3 HHHHHH 8

Search completed: March 21, 2006, 11:08:19
 Job time : 271 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:08:37 ; Search time 47 Seconds
(without alignments)
10.554 Million cell updates/sec

Title: US-10-719-523-5

Perfect score: 48

Sequence: 1 HHHHH 6

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5 COMB.pep:*
2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/prodata/1/1aa/H COMB.pep:*
4: /cgn2_6/prodata/1/1aa/ECTUS COMB.pep:*
5: /cgn2_6/prodata/1/1aa/RE COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	6	1	US-08-160-670A-6
2	48	100.0	6	1	US-08-140-222-1
3	48	100.0	6	1	US-08-131-365B-48
4	48	100.0	6	1	US-08-469-486-47
5	48	100.0	6	1	US-08-460-343B-51
6	48	100.0	6	1	US-08-299-567-1
7	48	100.0	6	1	US-08-398-028B-51
8	48	100.0	6	1	US-08-660-626-4
9	48	100.0	6	1	US-08-434-705B-17
10	48	100.0	6	1	US-08-470-837-22
11	48	100.0	6	1	US-08-472-244-14
12	48	100.0	6	1	US-08-504-265B-51
13	48	100.0	6	1	US-08-623-833B-16
14	48	100.0	6	1	US-08-652-507-8
15	48	100.0	6	1	US-08-668-123-48
16	48	100.0	6	1	US-08-469-658-47
17	48	100.0	6	1	US-09-086-201-17
18	48	100.0	6	1	US-08-591-196-57
19	48	100.0	6	2	US-08-996-139-18
20	48	100.0	6	2	US-08-481-435-42
21	48	100.0	6	2	US-08-772-440-28
22	48	100.0	6	2	US-09-267-031-18
23	48	100.0	6	2	US-09-398-341-1
24	48	100.0	6	2	US-09-031-168-4
25	48	100.0	6	2	US-08-789-333F-99
26	48	100.0	6	2	US-08-995-659-18
27	48	100.0	6	2	US-09-142-334-26

28	48	100.0	6	2	US-09-215-649A-18	Sequence 18, App1
29	48	100.0	6	2	US-09-140-084-7	Sequence 7, App1
30	48	100.0	6	2	US-09-382-950-4	Sequence 4, App1
31	48	100.0	6	2	US-08-382-736B-5	Sequence 5, App1
32	48	100.0	6	2	US-08-977-378-2	Sequence 2, App1
33	48	100.0	6	2	US-09-353-555-2	Sequence 2, App1
34	48	100.0	6	2	US-08-868-452-22	Sequence 22, App1
35	48	100.0	6	2	US-09-000-094-47	Sequence 47, App1
36	48	100.0	6	2	US-09-058-483-7	Sequence 7, App1
37	48	100.0	6	2	US-09-140-201-8	Sequence 8, App1
38	48	100.0	6	2	US-09-039-780A-106	Sequence 106, App
39	48	100.0	6	2	US-09-291-170A-14	Sequence 14, App1
40	48	100.0	6	2	US-09-577-780-18	Sequence 18, App1
41	48	100.0	6	2	US-09-724-297-7	Sequence 7, App1
42	48	100.0	6	2	US-09-367-309A-4	Sequence 4, App1
43	48	100.0	6	2	US-09-724-884-14	Sequence 14, App1
44	48	100.0	6	2	US-09-529-279-6	Sequence 6, App1
45	48	100.0	6	2	US-09-313-942-1	Sequence 1, App1
46	48	100.0	6	2	US-09-353-215-6	Sequence 6, App1
47	48	100.0	6	2	US-09-577-800-18	Sequence 18, App1
48	48	100.0	6	2	US-09-667-422-7	Sequence 7, App1
49	48	100.0	6	2	US-09-315-926A-81	Sequence 81, App1
50	48	100.0	6	2	US-09-731-558-11	Sequence 11, App1
51	48	100.0	6	2	US-09-280-030-61	Sequence 61, App1
52	48	100.0	6	2	US-09-466-496-18	Sequence 18, App1
53	48	100.0	6	2	US-09-648-569A-39	Sequence 39, App1
54	48	100.0	6	2	US-09-871-856-18	Sequence 18, App1
55	48	100.0	6	2	US-10-158-895-6	Sequence 6, App1
56	48	100.0	6	2	US-09-904-196B-9	Sequence 9, App1
57	48	100.0	6	2	US-09-871-291-19	Sequence 19, App1
58	48	100.0	6	2	US-09-115-397-1	Sequence 1, App1
59	48	100.0	6	2	US-09-463-194-2	Sequence 2, App1
60	48	100.0	6	2	US-09-353-554-1	Sequence 1, App1
61	48	100.0	6	2	US-09-669-516C-4	Sequence 4, App1
62	48	100.0	6	2	US-09-051-994-3	Sequence 3, App1
63	48	100.0	6	2	US-09-951-265-2	Sequence 2, App1
64	48	100.0	6	2	US-09-546-013-9	Sequence 9, App1
65	48	100.0	6	2	US-09-640-958-13	Sequence 13, App1
66	48	100.0	6	2	US-09-570-363-6	Sequence 6, App1
67	48	100.0	6	2	US-09-760-008A-9	Sequence 9, App1
68	48	100.0	6	2	US-09-877-650-18	Sequence 18, App1
69	48	100.0	6	2	US-09-596-794-20	Sequence 20, App1
70	48	100.0	6	2	US-09-970-989A-43	Sequence 43, App1
71	48	100.0	6	2	US-09-272-960-6	Sequence 6, App1
72	48	100.0	6	2	US-09-724-108-7	Sequence 7, App1
73	48	100.0	6	2	US-09-009-388C-7	Sequence 7, App1
74	48	100.0	6	2	US-10-058-636-6	Sequence 6, App1
75	48	100.0	6	2	US-09-974-992B-43	Sequence 43, App1
76	48	100.0	6	2	US-10-011-749-47	Sequence 47, App1
77	48	100.0	6	2	US-09-821-726A-19	Sequence 19, App1
78	48	100.0	6	2	US-09-916-949-99	Sequence 99, App1
79	48	100.0	6	2	US-09-826-312A-21	Sequence 21, App1
80	48	100.0	6	2	US-09-865-363-18	Sequence 18, App1
81	48	100.0	6	2	US-09-809-517A-11	Sequence 11, App1
82	48	100.0	6	2	US-09-943-382-1	Sequence 1, App1
83	48	100.0	6	2	US-09-352-171-3	Sequence 3, App1
84	48	100.0	6	2	US-10-452-786-1	Sequence 1, App1
85	48	100.0	6	2	US-09-288-718B-9	Sequence 9, App1
86	48	100.0	6	2	US-10-387-335-2	Sequence 2, App1
87	48	100.0	6	2	US-09-901-187C-13	Sequence 13, App1
88	48	100.0	6	2	US-09-043-861-36	Sequence 36, App1
89	48	100.0	6	2	US-09-692-945-15	Sequence 15, App1
90	48	100.0	6	2	US-09-782-587B-12	Sequence 12, App1
91	48	100.0	6	2	US-09-391-606-11	Sequence 11, App1
92	48	100.0	6	2	US-09-612-852A-17	Sequence 17, App1
93	48	100.0	6	2	US-09-989-981A-11	Sequence 11, App1
94	48	100.0	6	2	US-09-763-397A-26	Sequence 26, App1
95	48	100.0	6	2	US-10-192-294-9	Sequence 9, App1
96	48	100.0	6	2	US-09-688-459-18	Sequence 18, App1
97	48	100.0	6	2	US-09-979-338A-13	Sequence 13, App1
98	48	100.0	6	2	US-09-801-676A-2	Sequence 2, App1
99	48	100.0	6	2	US-09-935-430-688	Sequence 688, App
100	48	100.0	6	2	US-10-246-435-7	Sequence 7, App1

101	48	100.0	6	2	US-09-622-613C-43	Sequence 43, Appl	174	48	100.0	9	2	US-09-149-727-17	Sequence 17, Appl
102	48	100.0	6	2	US-09-673-222-14	Sequence 14, Appl	175	48	100.0	9	2	US-09-422-375-8	Sequence 8, Appl
103	48	100.0	6	2	US-09-813-197-5	Sequence 5, Appl	176	48	100.0	9	2	US-09-270-957-56	Sequence 56, Appl
104	48	100.0	6	2	US-09-962-756-1778	Sequence 1778, Ap	177	48	100.0	9	2	US-09-498-134A-9	Sequence 9, Appl
105	48	100.0	6	2	US-10-090-365-12	Sequence 12, Appl	178	48	100.0	9	2	US-09-809-517A-5	Sequence 5, Appl
106	48	100.0	6	2	US-10-093-248-10	Sequence 10, Appl	179	48	100.0	9	2	US-09-612-852A-16	Sequence 16, Appl
107	48	100.0	6	2	US-10-046-442-2	Sequence 2, Appl	180	48	100.0	9	2	US-10-665-227A-6	Sequence 6, Appl
108	48	100.0	6	2	US-09-728-911-12	Sequence 12, Appl	181	48	100.0	10	1	US-07-807-529A-73	Sequence 73, Appl
109	48	100.0	6	2	US-10-093-200A-10	Sequence 10, Appl	182	48	100.0	10	1	US-08-340-812-16	Sequence 16, Appl
110	48	100.0	6	2	US-10-665-227A-3	Sequence 3, Appl	183	48	100.0	10	1	US-08-459-064B-16	Sequence 16, Appl
111	48	100.0	6	2	US-10-282-162-1	Sequence 1, Appl	184	48	100.0	10	1	US-08-737-757-10	Sequence 10, Appl
112	48	100.0	6	2	US-09-997-623-41	Sequence 41, Appl	185	48	100.0	10	1	US-08-628-665-14	Sequence 14, Appl
113	48	100.0	6	2	US-10-346-658-1	Sequence 1, Appl	186	48	100.0	10	1	US-08-524-757-30	Sequence 30, Appl
114	48	100.0	6	2	US-10-317-252B-400	Sequence 400, App	187	48	100.0	10	1	US-08-524-757-30	Sequence 31, Appl
115	48	100.0	6	2	US-10-195-707B-35	Sequence 35, Appl	188	48	100.0	10	1	US-08-482-142-150	Sequence 150, App
116	48	100.0	6	4	PCR-US94-04361-55	Sequence 55, Appl	189	48	100.0	10	1	US-08-460-421A-16	Sequence 16, Appl
117	48	100.0	7	1	US-08-100-744-7	Sequence 7, Appl	190	48	100.0	10	1	US-08-717-169-13	Sequence 13, Appl
118	48	100.0	7	1	US-08-284-784-7	Sequence 7, Appl	191	48	100.0	10	1	US-08-220-240A-3	Sequence 3, Appl
119	48	100.0	7	1	US-08-854-811-7	Sequence 7, Appl	192	48	100.0	10	1	US-08-478-572-150	Sequence 150, App
120	48	100.0	7	2	US-08-865-468-9	Sequence 9, Appl	193	48	100.0	10	1	US-08-792-553-24	Sequence 24, App
121	48	100.0	7	2	US-09-216-430C-33	Sequence 33, Appl	194	48	100.0	10	2	US-08-300-928C-88	Sequence 88, Appl
122	48	100.0	7	2	US-09-809-517A-12	Sequence 12, Appl	195	48	100.0	10	2	US-08-430-944D-88	Sequence 88, Appl
123	48	100.0	7	2	US-09-809-517A-13	Sequence 13, Appl	196	48	100.0	10	2	US-08-430-014-88	Sequence 88, Appl
124	48	100.0	7	2	US-10-665-227A-4	Sequence 4, Appl	197	48	100.0	10	2	US-08-431-184-88	Sequence 88, Appl
125	48	100.0	8	1	US-08-762-433-6	Sequence 6, Appl	198	48	100.0	10	2	US-08-163-919A-17	Sequence 17, Appl
126	48	100.0	8	1	US-09-001-219-6	Sequence 6, Appl	199	48	100.0	10	2	US-08-639-294-9	Sequence 9, Appl
127	48	100.0	8	1	US-08-481-658B-22	Sequence 22, Appl	200	48	100.0	10	2	US-08-556-978B-10	Sequence 10, Appl
128	48	100.0	8	1	US-08-477-504A-22	Sequence 22, Appl	201	48	100.0	10	2	US-08-484-296-150	Sequence 150, App
129	48	100.0	8	1	US-08-486-756A-22	Sequence 22, Appl	202	48	100.0	10	2	US-09-425-638A-129	Sequence 129, App
130	48	100.0	8	1	US-08-485-862B-22	Sequence 22, Appl	203	48	100.0	10	2	US-09-543-004-129	Sequence 129, App
131	48	100.0	8	2	US-08-787-739-22	Sequence 22, Appl	204	48	100.0	10	2	US-09-039-780A-101	Sequence 101, App
132	48	100.0	8	2	US-08-817-732A-40	Sequence 40, Appl	205	48	100.0	10	2	US-09-099-053-27	Sequence 27, Appl
133	48	100.0	8	2	US-08-487-077A-22	Sequence 22, Appl	206	48	100.0	10	2	US-09-228-901A-13	Sequence 13, Appl
134	48	100.0	8	2	US-08-816-977-11	Sequence 11, Appl	207	48	100.0	10	2	US-08-981-490B-5	Sequence 5, Appl
135	48	100.0	8	2	US-08-485-863A-22	Sequence 22, Appl	208	48	100.0	10	2	US-09-861-034B-9	Sequence 9, Appl
136	48	100.0	8	2	US-08-485-049D-22	Sequence 22, Appl	209	48	100.0	10	2	US-08-462-515-17	Sequence 17, Appl
137	48	100.0	8	2	US-08-556-978B-13	Sequence 13, Appl	210	48	100.0	10	2	US-09-809-517A-2	Sequence 2, Appl
138	48	100.0	8	2	US-08-637-732A-40	Sequence 40, Appl	211	48	100.0	10	2	US-09-015-399-13	Sequence 13, Appl
139	48	100.0	8	2	US-08-817-787-31	Sequence 31, Appl	212	48	100.0	10	2	US-09-015-399-11	Sequence 11, Appl
140	48	100.0	8	2	US-09-178-115-22	Sequence 22, Appl	213	48	100.0	10	2	US-08-594-575C-24	Sequence 24, Appl
141	48	100.0	8	2	US-09-177-776-22	Sequence 22, Appl	214	48	100.0	10	2	US-09-402-131-9	Sequence 9, Appl
142	48	100.0	8	2	US-09-549-831-15	Sequence 15, Appl	215	48	100.0	10	2	US-10-188-347-1	Sequence 1, Appl
143	48	100.0	8	2	US-09-326-529-16	Sequence 16, Appl	216	48	100.0	10	2	US-10-665-227A-7	Sequence 7, Appl
144	48	100.0	8	2	US-09-464-152A-14	Sequence 14, Appl	217	48	100.0	10	2	US-10-048-882C-3	Sequence 3, Appl
145	48	100.0	8	2	US-09-648-569A-40	Sequence 40, Appl	218	48	100.0	10	4	PCR-US93-00909-13	Sequence 13, Appl
146	48	100.0	8	2	US-09-904-196B-10	Sequence 10, Appl	219	48	100.0	10	4	PCR-US94-14073-17	Sequence 17, Appl
147	48	100.0	8	2	US-09-760-008A-10	Sequence 10, Appl	220	48	100.0	10	4	PCR-US95-04439-9	Sequence 9, Appl
148	48	100.0	8	2	US-09-334-477-11	Sequence 11, Appl	221	48	100.0	11	1	US-08-133-804-11	Sequence 11, Appl
149	48	100.0	8	2	US-09-583-808-31	Sequence 31, Appl	222	48	100.0	11	1	US-08-461-838-11	Sequence 11, Appl
150	48	100.0	8	2	US-09-772-719B-22	Sequence 22, Appl	223	48	100.0	11	1	US-08-737-757-4	Sequence 4, Appl
151	48	100.0	8	2	US-08-260-190-22	Sequence 22, Appl	224	48	100.0	11	1	US-08-461-366-11	Sequence 11, Appl
152	48	100.0	8	2	US-09-786-442B-18	Sequence 18, Appl	225	48	100.0	11	2	US-09-814-569-2	Sequence 2, Appl
153	48	100.0	8	2	US-09-589-483-28	Sequence 28, Appl	226	48	100.0	11	2	US-09-515-534A-8	Sequence 8, Appl
154	48	100.0	8	2	US-09-782-587B-13	Sequence 13, Appl	227	48	100.0	11	2	US-09-319-806-8	Sequence 8, Appl
155	48	100.0	8	2	US-09-319-806-7	Sequence 7, Appl	228	48	100.0	11	2	US-10-665-227A-8	Sequence 8, Appl
156	48	100.0	8	2	US-10-192-294-10	Sequence 10, Appl	229	48	100.0	12	1	US-08-100-744-11	Sequence 11, Appl
157	48	100.0	8	2	US-09-244-984-2	Sequence 2, Appl	230	48	100.0	12	1	US-08-284-784-11	Sequence 11, Appl
158	48	100.0	8	2	US-09-589-777C-20	Sequence 20, Appl	231	48	100.0	12	1	US-08-459-064B-35	Sequence 35, Appl
159	48	100.0	8	2	US-10-665-227A-5	Sequence 5, Appl	232	48	100.0	12	1	US-08-460-421A-35	Sequence 35, Appl
160	48	100.0	8	2	US-09-997-623-42	Sequence 42, Appl	233	48	100.0	12	1	US-08-854-811-11	Sequence 11, Appl
161	48	100.0	8	2	US-10-195-707B-36	Sequence 36, Appl	234	48	100.0	12	1	US-09-331-362-10	Sequence 10, Appl
162	48	100.0	9	1	US-08-155-171B-4	Sequence 4, Appl	235	48	100.0	12	2	US-08-327-874A-4	Sequence 4, Appl
163	48	100.0	9	1	US-08-100-744-12	Sequence 12, Appl	236	48	100.0	12	2	US-09-266-498-7	Sequence 7, Appl
164	48	100.0	9	1	US-08-284-784-12	Sequence 12, Appl	237	48	100.0	12	2	US-09-376-330-6	Sequence 6, Appl
165	48	100.0	9	1	US-08-737-757-12	Sequence 12, Appl	238	48	100.0	12	2	US-09-395-017B-36	Sequence 36, Appl
166	48	100.0	9	1	US-08-854-811-12	Sequence 12, Appl	239	48	100.0	12	2	US-09-643-657-43	Sequence 43, Appl
167	48	100.0	9	1	US-08-435-998-4	Sequence 4, Appl	240	48	100.0	12	2	US-09-601-040A-13	Sequence 13, Appl
168	48	100.0	9	2	US-09-143-470-19	Sequence 19, Appl	241	48	100.0	12	2	US-10-008-960-4	Sequence 4, Appl
169	48	100.0	9	2	US-09-254-567-1	Sequence 1, Appl	242	48	100.0	12	2	US-09-921-992-83	Sequence 83, Appl
170	48	100.0	9	2	US-08-895-707-9	Sequence 9, Appl	243	48	100.0	12	2	US-09-715-836A-10	Sequence 10, Appl
171	48	100.0	9	2	US-08-875-533-36	Sequence 36, Appl	244	48	100.0	12	2	US-09-566-470A-3	Sequence 3, Appl
172	48	100.0	9	2	US-08-556-978B-102	Sequence 102, App	245	48	100.0	12	2	US-10-665-227A-9	Sequence 9, Appl
173	48	100.0	9	2	US-09-076-804-1	Sequence 1, Appl	246	48	100.0	12	2	US-09-269-874A-8	Sequence 8, Appl

247	48	100.0	12	4	PCT-US94-09700-4	Sequence 4, Appl1	320	48	100.0	17	2	US-09-809-517A-32	Sequence 32, Appl1
248	48	100.0	13	1	US-08-571-643A-4	Sequence 4, Appl1	321	48	100.0	17	4	PCT-US94-01176-19	Sequence 19, Appl1
249	48	100.0	13	1	US-08-439-747A-22	Sequence 22, Appl1	322	48	100.0	18	1	US-08-145-006C-6	Sequence 6, Appl1
250	48	100.0	13	1	US-08-482-577B-15	Sequence 15, Appl1	323	48	100.0	18	1	US-08-578-649-14	Sequence 14, Appl1
251	48	100.0	13	1	US-08-440-409B-22	Sequence 22, Appl1	324	48	100.0	18	1	US-08-356-068A-47	Sequence 47, Appl1
252	48	100.0	13	2	US-08-981-321-8	Sequence 8, Appl1	325	48	100.0	18	1	US-08-670-175-8	Sequence 8, Appl1
253	48	100.0	13	2	US-09-218-176-40	Sequence 40, Appl1	326	48	100.0	18	2	US-08-895-707-15	Sequence 15, Appl1
254	48	100.0	13	2	US-09-331-362-8	Sequence 8, Appl1	327	48	100.0	18	2	US-08-460-900C-47	Sequence 47, Appl1
255	48	100.0	13	2	US-08-556-978B-40	Sequence 40, Appl1	328	48	100.0	18	2	US-08-460-900C-61	Sequence 61, Appl1
256	48	100.0	13	2	US-09-147-805-7	Sequence 7, Appl1	329	48	100.0	18	2	US-08-674-509B-47	Sequence 47, Appl1
257	48	100.0	13	2	US-09-418-785-3	Sequence 3, Appl1	330	48	100.0	18	2	US-08-954-698-47	Sequence 47, Appl1
258	48	100.0	13	2	US-09-116-492A-32	Sequence 32, Appl1	331	48	100.0	18	2	US-08-957-874-47	Sequence 47, Appl1
259	48	100.0	13	2	US-09-863-859-20	Sequence 20, Appl1	332	48	100.0	18	2	US-09-400-816-1	Sequence 1, Appl1
260	48	100.0	13	2	US-09-823-266-2	Sequence 2, Appl1	333	48	100.0	18	2	US-09-429-370-45	Sequence 45, Appl1
261	48	100.0	13	2	US-09-823-266-3	Sequence 3, Appl1	334	48	100.0	18	2	US-09-639-695-47	Sequence 47, Appl1
262	48	100.0	13	2	US-09-823-266-4	Sequence 4, Appl1	335	48	100.0	18	2	US-09-639-695-61	Sequence 61, Appl1
263	48	100.0	13	2	US-09-823-266-5	Sequence 5, Appl1	336	48	100.0	18	2	US-09-448-188-47	Sequence 47, Appl1
264	48	100.0	13	2	US-10-188-602-1	Sequence 1, Appl1	337	48	100.0	18	2	US-08-954-128-47	Sequence 47, Appl1
265	48	100.0	13	2	US-10-155-419-2	Sequence 2, Appl1	338	48	100.0	18	2	US-08-954-1740-47	Sequence 47, Appl1
266	48	100.0	13	2	US-10-155-419-3	Sequence 3, Appl1	339	48	100.0	18	2	US-09-395-017B-48	Sequence 48, Appl1
267	48	100.0	13	2	US-10-155-419-4	Sequence 4, Appl1	340	48	100.0	18	2	US-09-795-872-1	Sequence 1, Appl1
268	48	100.0	13	2	US-10-155-419-5	Sequence 5, Appl1	341	48	100.0	18	2	US-09-736-476-47	Sequence 47, Appl1
269	48	100.0	14	1	US-07-807-529A-76	Sequence 76, Appl1	342	48	100.0	18	2	US-09-809-517A-1	Sequence 1, Appl1
270	48	100.0	14	1	US-08-226-264-7	Sequence 7, Appl1	343	48	100.0	18	4	PCT-US94-00545-6	Sequence 6, Appl1
271	48	100.0	14	1	US-08-226-264-19	Sequence 19, Appl1	344	48	100.0	19	2	US-09-167-434-15	Sequence 15, Appl1
272	48	100.0	14	1	US-08-226-264-20	Sequence 20, Appl1	345	48	100.0	19	2	US-08-853-755-15	Sequence 15, Appl1
273	48	100.0	14	1	US-08-448-418-100	Sequence 100, App	346	48	100.0	19	2	US-09-129-192C-72	Sequence 72, Appl1
274	48	100.0	14	1	US-08-467-603-58	Sequence 58, Appl1	347	48	100.0	19	2	US-09-933-999A-31	Sequence 31, Appl1
275	48	100.0	14	1	US-08-466-793-58	Sequence 58, Appl1	348	48	100.0	20	1	US-08-373-134D-3	Sequence 3, Appl1
276	48	100.0	14	1	US-08-491-861A-58	Sequence 58, Appl1	349	48	100.0	20	1	US-08-416-336-4	Sequence 4, Appl1
277	48	100.0	14	2	US-08-300-928C-91	Sequence 91, Appl1	350	48	100.0	20	1	US-08-543-020-12	Sequence 12, Appl1
278	48	100.0	14	2	US-08-430-944D-91	Sequence 91, Appl1	351	48	100.0	20	1	US-09-114-637-3	Sequence 3, Appl1
279	48	100.0	14	2	US-08-430-014-91	Sequence 91, Appl1	352	48	100.0	20	2	US-08-542-051-21	Sequence 21, Appl1
280	48	100.0	14	2	US-08-956-307B-3	Sequence 3, Appl1	353	48	100.0	20	2	US-08-485-942A-99	Sequence 99, Appl1
281	48	100.0	14	2	US-08-431-184-91	Sequence 91, Appl1	354	48	100.0	20	2	US-08-488-214A-99	Sequence 99, Appl1
282	48	100.0	14	2	US-09-374-671A-58	Sequence 58, Appl1	355	48	100.0	20	2	US-08-640-737-32	Sequence 32, Appl1
283	48	100.0	14	2	US-09-146-979-100	Sequence 100, App	356	48	100.0	20	2	US-09-186-489-6	Sequence 6, Appl1
284	48	100.0	14	2	US-09-623-326-16	Sequence 16, Appl1	357	48	100.0	20	2	US-08-122-458D-7	Sequence 7, Appl1
285	48	100.0	14	2	US-09-823-266-1	Sequence 1, Appl1	358	48	100.0	20	2	US-08-438-431A-99	Sequence 99, Appl1
286	48	100.0	14	2	US-09-388-316C-30	Sequence 30, Appl1	359	48	100.0	20	2	US-09-638-202A-114	Sequence 114, App
287	48	100.0	14	2	US-10-004-381-32	Sequence 32, Appl1	360	48	100.0	20	2	US-09-096-724B-34	Sequence 34, Appl1
288	48	100.0	14	2	US-10-155-419-1	Sequence 1, Appl1	361	48	100.0	20	2	US-09-674-677-34	Sequence 34, Appl1
289	48	100.0	15	1	US-08-469-480-58	Sequence 48, Appl1	362	48	100.0	20	2	US-10-043-665B-6	Sequence 6, Appl1
290	48	100.0	15	1	US-08-467-603-53	Sequence 53, Appl1	363	48	100.0	20	2	US-09-623-326-14	Sequence 14, Appl1
291	48	100.0	15	1	US-08-466-793-53	Sequence 53, Appl1	364	48	100.0	20	2	US-09-096-749A-114	Sequence 114, App
292	48	100.0	15	1	US-08-469-658-48	Sequence 48, Appl1	365	48	100.0	20	2	US-09-637-614-114	Sequence 114, App
293	48	100.0	15	1	US-08-491-861A-53	Sequence 53, Appl1	366	48	100.0	20	2	US-09-612-314A-48	Sequence 48, Appl1
294	48	100.0	15	2	US-09-374-671A-53	Sequence 53, Appl1	367	48	100.0	20	2	US-10-420-564-6	Sequence 6, Appl1
295	48	100.0	15	2	US-10-015-328-2	Sequence 2, Appl1	368	48	100.0	20	2	US-09-935-280B-19	Sequence 19, Appl1
296	48	100.0	15	2	US-09-728-653-2	Sequence 2, Appl1	369	48	100.0	20	2	US-09-486-480-5	Sequence 5, Appl1
297	48	100.0	15	2	US-09-921-992-85	Sequence 85, Appl1	370	48	100.0	21	1	US-08-432-871C-46	Sequence 46, Appl1
298	48	100.0	15	2	US-09-506-078-37	Sequence 37, Appl1	371	48	100.0	21	1	US-08-651-818A-21	Sequence 21, Appl1
299	48	100.0	15	2	US-10-221-655A-5	Sequence 5, Appl1	372	48	100.0	21	1	US-08-712-878-6	Sequence 6, Appl1
300	48	100.0	16	1	US-08-578-649-13	Sequence 13, Appl1	373	48	100.0	21	2	US-08-485-942A-98	Sequence 98, Appl1
301	48	100.0	16	1	US-08-226-264-8	Sequence 8, Appl1	374	48	100.0	21	2	US-08-488-214A-98	Sequence 98, Appl1
302	48	100.0	16	1	US-08-226-264-21	Sequence 21, Appl1	375	48	100.0	21	2	US-08-488-208A-98	Sequence 98, Appl1
303	48	100.0	16	2	US-08-706-945D-145	Sequence 145, App	376	48	100.0	21	2	US-09-071-710-41	Sequence 41, Appl1
304	48	100.0	16	2	US-09-039-780A-103	Sequence 103, App	377	48	100.0	21	2	US-08-912-276-25	Sequence 25, Appl1
305	48	100.0	16	2	US-09-039-780A-105	Sequence 105, App	378	48	100.0	21	2	US-09-153-804-17	Sequence 17, Appl1
306	48	100.0	16	2	US-09-367-309A-3	Sequence 3, Appl1	379	48	100.0	21	2	US-08-944-483-76	Sequence 76, Appl1
307	48	100.0	16	2	US-09-506-768-15	Sequence 15, Appl1	380	48	100.0	21	2	US-09-184-826-21	Sequence 21, Appl1
308	48	100.0	16	2	US-09-822-765A-1	Sequence 1, Appl1	381	48	100.0	21	2	US-09-525-397-41	Sequence 41, Appl1
309	48	100.0	16	2	US-09-809-517A-4	Sequence 4, Appl1	382	48	100.0	21	2	US-08-483-211A-98	Sequence 98, Appl1
310	48	100.0	16	2	US-09-809-517A-29	Sequence 29, Appl1	383	48	100.0	21	2	US-09-566-876-16	Sequence 16, Appl1
311	48	100.0	17	1	US-09-645-415A-23	Sequence 23, Appl1	384	48	100.0	21	2	US-08-488-223A-98	Sequence 98, Appl1
312	48	100.0	17	1	US-08-021-603A-19	Sequence 19, Appl1	385	48	100.0	21	2	US-09-049-696-51	Sequence 51, Appl1
313	48	100.0	17	1	US-08-155-171B-37	Sequence 37, Appl1	386	48	100.0	21	2	US-09-065-383-33	Sequence 33, Appl1
314	48	100.0	17	1	US-08-435-998-37	Sequence 37, Appl1	387	48	100.0	21	2	US-08-438-431A-98	Sequence 98, Appl1
315	48	100.0	17	1	US-08-600-783-13	Sequence 13, Appl1	388	48	100.0	21	2	US-09-270-956-46	Sequence 46, Appl1
316	48	100.0	17	2	US-08-946-475-10	Sequence 10, Appl1	389	48	100.0	21	2	US-09-276-600-11	Sequence 11, Appl1
317	48	100.0	17	2	US-09-136-421-10	Sequence 10, Appl1	390	48	100.0	21	2	US-08-488-225A-98	Sequence 98, Appl1
318	48	100.0	17	2	US-09-340-479-10	Sequence 10, Appl1	391	48	100.0	21	2	US-09-193-881-29	Sequence 29, Appl1
319	48	100.0	17	2	US-09-230-846A-5	Sequence 5, Appl1	392	48	100.0	21	2	US-09-689-065B-104	Sequence 104, App

333	48	100.0	21	2	US-09-050-516-49	Sequence 49, Appl	466	48	100.0	29	2	US-09-419-381-47	Sequence 47, Appl
334	48	100.0	21	2	US-09-939-126-8	Sequence 8, Appl.i	467	48	100.0	29	2	US-09-419-381-48	Sequence 48, Appl
335	48	100.0	21	2	US-09-939-126-9	Sequence 9, Appl.i	468	48	100.0	29	2	US-09-880-901-2	Sequence 2, Appl
336	48	100.0	21	2	US-09-939-126-10	Sequence 10, Appl	469	48	100.0	29	2	US-09-962-756-2202	Sequence 2202, Ap
337	48	100.0	21	2	US-09-939-126-11	Sequence 11, Appl	470	48	100.0	29	2	US-09-486-480-7	Sequence 7, Appl
338	48	100.0	21	2	US-09-939-126-12	Sequence 12, Appl	471	48	100.0	29	4	PCR-US94-05150-37	Sequence 37, Appl
339	48	100.0	21	2	US-10-278-547-49	Sequence 49, Appl	472	48	100.0	30	2	US-09-039-780A-98	Sequence 98, Appl
340	48	100.0	21	2	US-09-431-384B-31	Sequence 31, Appl	473	48	100.0	30	2	US-09-039-780A-100	Sequence 100, App
401	48	100.0	21	2	US-09-589-483-15	Sequence 15, Appl	474	48	100.0	30	2	US-09-039-780A-104	Sequence 104, App
402	48	100.0	21	2	US-09-589-483-29	Sequence 29, Appl	475	48	100.0	30	2	US-09-150-867-11	Sequence 11, Appl
403	48	100.0	21	2	US-09-832-464-21	Sequence 21, Appl	476	48	100.0	31	1	US-08-662-227-37	Sequence 37, Appl
404	48	100.0	21	2	US-10-010-160-68	Sequence 68, Appl	477	48	100.0	31	2	US-09-017-947-37	Sequence 37, Appl
405	48	100.0	21	2	US-09-173-713-5	Sequence 5, Appl.i	478	48	100.0	31	2	US-09-925-442-37	Sequence 37, Appl
406	48	100.0	21	2	US-09-589-777C-7	Sequence 7, Appl.i	479	48	100.0	31	2	US-09-897-776A-35	Sequence 35, Appl
407	48	100.0	21	2	US-09-052-855A-10	Sequence 30, Appl	480	48	100.0	31	2	US-09-962-756-2203	Sequence 2203, Ap
408	48	100.0	21	2	US-09-080-140-31	Sequence 31, Appl	481	48	100.0	32	2	US-08-737-336-1	Sequence 1, Appl
409	48	100.0	21	2	US-09-092-297A-32	Sequence 22, Appl	482	48	100.0	33	2	US-09-897-776A-28	Sequence 28, Appl
410	48	100.0	22	2	US-09-039-780A-102	Sequence 102, App	483	48	100.0	33	2	US-09-866-538-21	Sequence 21, Appl
411	48	100.0	22	2	US-09-660-742-3	Sequence 3, Appl.i	484	48	100.0	33	2	US-10-346-658-2	Sequence 2, Appl
412	48	100.0	23	1	US-08-480-604A-24	Sequence 24, Appl	485	48	100.0	33	2	US-09-839-577A-6	Sequence 6, Appl.i
413	48	100.0	23	1	US-08-273-146-37	Sequence 37, Appl	486	48	100.0	33	2	US-09-839-577A-7	Sequence 7, Appl.i
414	48	100.0	23	1	US-08-405-496A-24	Sequence 24, Appl	487	48	100.0	35	2	US-09-962-756-2204	Sequence 2204, Ap
415	48	100.0	23	1	US-08-350-260A-42	Sequence 42, Appl	488	48	100.0	37	2	US-09-507-333B-10	Sequence 10, Appl
416	48	100.0	23	2	US-08-762-483-7	Sequence 7, Appl.i	489	48	100.0	37	2	US-09-039-780A-97	Sequence 97, Appl
417	48	100.0	23	2	US-08-913-136-24	Sequence 24, Appl	490	48	100.0	37	2	US-09-575-867-5	Sequence 5, Appl.i
418	48	100.0	23	2	US-09-660-742-5	Sequence 5, Appl.i	491	48	100.0	37	2	US-09-084-303B-283	Sequence 283, App
419	48	100.0	23	2	US-09-104-337A-42	Sequence 42, Appl	492	48	100.0	37	2	US-10-094-944-15	Sequence 15, Appl
420	48	100.0	23	2	US-09-084-517-24	Sequence 24, Appl	493	48	100.0	38	2	US-09-962-756-2069	Sequence 2069, Ap
421	48	100.0	23	2	US-09-939-126-7	Sequence 7, Appl.i	494	48	100.0	38	2	US-09-839-577A-12	Sequence 12, Appl
422	48	100.0	23	2	US-09-897-776A-31	Sequence 31, Appl	495	48	100.0	39	1	US-08-679-865-39	Sequence 39, Appl
423	48	100.0	23	2	US-09-589-483-30	Sequence 30, Appl	496	48	100.0	39	1	US-08-680-876-39	Sequence 39, Appl
424	48	100.0	23	2	US-09-589-777C-23	Sequence 23, Appl	497	48	100.0	39	2	US-09-263-975-39	Sequence 39, Appl
425	48	100.0	24	1	US-08-021-603A-16	Sequence 16, Appl	498	48	100.0	39	2	US-09-450-072-78	Sequence 78, Appl
426	48	100.0	24	1	US-08-584-031-8	Sequence 8, Appl.i	499	48	100.0	39	2	US-09-351-348-78	Sequence 78, Appl
427	48	100.0	24	2	US-08-780-496-8	Sequence 8, Appl.i	500	48	100.0	40	1	US-08-273-146-39	Sequence 39, Appl
428	48	100.0	24	2	US-09-507-323B-9	Sequence 9, Appl.i	501	48	100.0	41	2	US-09-129-192C-70	Sequence 70, Appl
429	48	100.0	24	2	US-09-556-877-221	Sequence 221, App	502	48	100.0	42	1	US-08-664-449-39	Sequence 39, Appl
430	48	100.0	24	2	US-09-620-412C-221	Sequence 221, App	503	48	100.0	42	2	US-09-309-382-12	Sequence 12, Appl
431	48	100.0	24	2	US-09-292-858B-27	Sequence 27, Appl	504	48	100.0	42	2	US-09-510-031A-3	Sequence 3, Appl.i
432	48	100.0	24	2	US-08-928-069-9	Sequence 9, Appl.i	505	48	100.0	43	1	US-08-273-146-41	Sequence 41, Appl
433	48	100.0	24	2	US-09-598-419-221	Sequence 221, App	506	48	100.0	43	1	US-08-652-816A-43	Sequence 43, Appl
434	48	100.0	24	2	US-09-582-450-8	Sequence 8, Appl.i	507	48	100.0	43	1	US-08-347-563A-12	Sequence 12, Appl
435	48	100.0	24	2	US-09-934-465-8	Sequence 8, Appl.i	508	48	100.0	43	2	US-08-485-942A-12	Sequence 12, Appl
436	48	100.0	24	2	US-09-589-483-14	Sequence 14, Appl	509	48	100.0	43	2	US-08-488-214A-12	Sequence 12, Appl
437	48	100.0	24	2	US-09-589-777C-5	Sequence 5, Appl.i	510	48	100.0	43	2	US-08-488-208A-12	Sequence 12, Appl
438	48	100.0	24	4	PCR-US94-01176-16	Sequence 16, Appl	511	48	100.0	43	2	US-08-483-211A-12	Sequence 12, Appl
439	48	100.0	25	2	US-09-039-780A-96	Sequence 96, Appl	512	48	100.0	43	2	US-08-488-223A-12	Sequence 12, Appl
440	48	100.0	25	2	US-09-721-154-14	Sequence 14, Appl	513	48	100.0	43	2	US-08-438-431A-12	Sequence 12, Appl
441	48	100.0	25	2	US-09-897-776A-22	Sequence 22, Appl	514	48	100.0	43	2	US-08-488-225A-12	Sequence 12, Appl
442	48	100.0	25	2	US-10-381-846-5	Sequence 5, Appl.i	515	48	100.0	43	2	US-09-686-647A-12	Sequence 12, Appl
443	48	100.0	26	1	US-08-227-372-2	Sequence 2, Appl.i	516	48	100.0	43	2	US-09-962-756-2111	Sequence 2111, Ap
444	48	100.0	26	1	US-08-657-641-12	Sequence 12, Appl	517	48	100.0	43	2	US-08-896-535-62	Sequence 62, Appl
445	48	100.0	26	2	US-08-470-397-2	Sequence 2, Appl.i	518	48	100.0	44	1	US-08-652-507-6	Sequence 6, Appl
446	48	100.0	26	2	US-08-895-707-21	Sequence 21, Appl	519	48	100.0	44	2	US-09-039-780A-99	Sequence 99, Appl
447	48	100.0	26	2	US-09-897-776A-25	Sequence 25, Appl	520	48	100.0	44	2	US-09-419-381-121	Sequence 121, App
448	48	100.0	26	2	US-09-589-483-17	Sequence 17, Appl	521	48	100.0	44	2	US-09-921-144-8	Sequence 8, Appl
449	48	100.0	26	2	US-09-589-777C-13	Sequence 13, Appl	522	48	100.0	44	2	US-10-317-252B-296	Sequence 296, App
450	48	100.0	26	2	US-09-486-480-6	Sequence 6, Appl.i	523	48	100.0	45	2	US-09-921-144-6	Sequence 6, Appl
451	48	100.0	26	4	PCR-US94-07233-12	Sequence 12, Appl	524	48	100.0	45	2	US-10-010-160-61	Sequence 61, Appl
452	48	100.0	27	2	US-09-411-329C-32	Sequence 32, Appl	525	48	100.0	48	1	US-08-457-245-21	Sequence 21, Appl
453	48	100.0	27	2	US-09-411-329C-26	Sequence 26, Appl	526	48	100.0	48	2	US-09-419-381-120	Sequence 120, App
454	48	100.0	27	2	US-09-846-729A-42	Sequence 22, Appl	527	48	100.0	48	2	US-09-921-144-8	Sequence 8, Appl
455	48	100.0	27	2	US-09-846-729A-26	Sequence 26, Appl	528	48	100.0	48	2	US-10-158-742A-15	Sequence 15, Appl
456	48	100.0	27	2	US-09-898-461-9	Sequence 9, Appl.i	529	48	100.0	49	2	US-09-979-338A-26	Sequence 26, Appl
457	48	100.0	28	2	US-08-978-741-14	Sequence 14, Appl	530	48	100.0	49	2	US-10-084-298-10	Sequence 10, Appl
458	48	100.0	28	2	US-09-333-729A-14	Sequence 14, Appl	531	48	100.0	50	2	US-09-507-333B-11	Sequence 11, Appl
459	48	100.0	28	2	US-09-897-776A-20	Sequence 20, Appl	532	48	100.0	50	2	US-09-360-237-53	Sequence 53, Appl
460	48	100.0	29	2	US-09-419-381-41	Sequence 41, Appl	533	48	100.0	50	2	US-10-010-160-64	Sequence 64, Appl
461	48	100.0	29	2	US-09-419-381-42	Sequence 42, Appl	534	48	100.0	51	2	US-10-158-742A-14	Sequence 14, Appl
462	48	100.0	29	2	US-09-419-381-43	Sequence 43, Appl	535	48	100.0	51	2	US-08-978-741-15	Sequence 15, Appl
463	48	100.0	29	2	US-09-419-381-44	Sequence 44, Appl	536	48	100.0	52	2	US-09-333-729A-13	Sequence 13, Appl
464	48	100.0	29	2	US-09-419-381-45	Sequence 45, Appl	537	48	100.0	52	2	US-10-158-742A-13	Sequence 13, Appl
465	48	100.0	29	2	US-09-419-381-46	Sequence 46, Appl	538	48	100.0	53	1	US-08-651-818A-19	Sequence 19, Appl

539	48	100.0	53	2	US-09-184-826-19	Sequence 19, Appl	612	48	100.0	95	2	US-09-270-767-57350	Sequence 57350, A
540	48	100.0	53	2	US-09-832-464-19	Sequence 19, Appl	613	48	100.0	95	2	US-09-270-767-60865	Sequence 60865, A
541	48	100.0	54	1	US-08-651-818A-23	Sequence 23, Appl	614	48	100.0	96	1	US-07-807-529A-39	Sequence 39, Appl
542	48	100.0	54	2	US-09-184-826-23	Sequence 23, Appl	615	48	100.0	96	2	US-08-430-944D-103	Sequence 103, App
543	48	100.0	54	2	US-09-832-464-23	Sequence 23, Appl	616	48	100.0	96	2	US-08-431-184-103	Sequence 103, App
544	48	100.0	54	2	US-10-158-742A-11	Sequence 11, Appl	617	48	100.0	96	2	US-09-636-215-827	Sequence 827, App
545	48	100.0	54	2	US-10-158-742A-12	Sequence 12, Appl	618	48	100.0	96	2	US-09-685-166A-827	Sequence 827, App
546	48	100.0	57	1	US-08-652-816A-41	Sequence 41, Appl	619	48	100.0	96	2	US-09-679-426-827	Sequence 827, App
547	48	100.0	57	1	US-08-958-201-18	Sequence 18, Appl	620	48	100.0	96	2	US-09-759-143-827	Sequence 827, App
548	48	100.0	57	2	US-09-979-338A-23	Sequence 23, Appl	621	48	100.0	96	2	US-09-651-236-827	Sequence 827, App
549	48	100.0	57	2	US-09-979-338A-29	Sequence 29, Appl	622	48	100.0	96	2	US-09-657-272-827	Sequence 827, App
550	48	100.0	58	2	US-10-158-742A-2	Sequence 2, Appl1	623	48	100.0	96	2	US-10-012-896-827	Sequence 827, App
551	48	100.0	60	1	US-08-255-457-1	Sequence 1, Appl1	624	48	100.0	97	2	US-08-816-977-23	Sequence 23, Appl
552	48	100.0	60	1	US-09-115-032-1	Sequence 1, Appl1	625	48	100.0	97	2	US-08-816-977-27	Sequence 27, Appl
553	48	100.0	60	2	US-09-076-804-4	Sequence 4, Appl1	626	48	100.0	97	2	US-09-174-943-2	Sequence 2, Appl1
554	48	100.0	60	4	PCR-US95-05772-1	Sequence 1, Appl1	627	48	100.0	97	2	US-09-334-477-23	Sequence 23, Appl
555	48	100.0	62	4	US-10-017-754-1880	Sequence 1880, Ap	628	48	100.0	97	2	US-09-334-477-27	Sequence 27, Appl
556	48	100.0	64	2	US-09-601-537-17	Sequence 17, Appl	629	48	100.0	99	2	US-09-407-687-43	Sequence 43, Appl
557	48	100.0	67	1	US-08-142-551B-9	Sequence 9, Appl1	630	48	100.0	101	2	US-10-263-103-31	Sequence 31, Appl
558	48	100.0	67	2	US-09-268-070-3	Sequence 3, Appl1	631	48	100.0	103	2	US-10-263-103-29	Sequence 29, Appl
559	48	100.0	67	2	US-09-921-144-10	Sequence 10, Appl	632	48	100.0	103	2	US-10-263-103-32	Sequence 32, Appl
560	48	100.0	68	2	US-09-268-070-1	Sequence 1, Appl1	633	48	100.0	105	2	US-10-263-103-26	Sequence 26, Appl
561	48	100.0	68	2	US-09-174-943-6	Sequence 6, Appl1	634	48	100.0	105	2	US-10-263-103-30	Sequence 30, Appl
562	48	100.0	68	2	US-09-979-338A-25	Sequence 25, Appl	635	48	100.0	108	2	US-10-263-103-33	Sequence 33, Appl
563	48	100.0	69	1	US-08-687-865A-21	Sequence 21, Appl	636	48	100.0	108	2	US-09-473-551-15	Sequence 15, Appl
564	48	100.0	69	2	US-09-268-070-2	Sequence 2, Appl1	637	48	100.0	109	2	US-09-407-687-41	Sequence 41, Appl
565	48	100.0	69	2	US-09-043-711-21	Sequence 21, Appl	638	48	100.0	109	2	US-09-979-338A-28	Sequence 28, Appl
566	48	100.0	70	2	US-09-921-144-12	Sequence 12, Appl	639	48	100.0	109	2	US-09-473-551-11	Sequence 11, Appl
567	48	100.0	71	2	US-09-146-054-9	Sequence 9, Appl1	640	48	100.0	109	2	US-09-473-551-13	Sequence 13, Appl
568	48	100.0	71	2	US-09-664-977A-9	Sequence 9, Appl1	641	48	100.0	110	1	US-08-434-705B-15	Sequence 15, Appl
569	48	100.0	72	2	US-09-042-071-38	Sequence 38, Appl	642	48	100.0	110	1	US-09-086-201-15	Sequence 15, Appl
570	48	100.0	73	2	US-09-979-338A-30	Sequence 30, Appl	643	48	100.0	111	2	US-09-622-613C-9	Sequence 9, Appl1
571	48	100.0	74	2	US-09-490-291-11	Sequence 11, Appl	644	48	100.0	112	2	US-08-728-742A-56	Sequence 56, Appl
572	48	100.0	76	2	US-08-956-307B-17	Sequence 17, Appl	645	48	100.0	113	2	US-09-581-894A-11	Sequence 11, Appl
573	48	100.0	76	2	US-08-356-307B-18	Sequence 18, Appl	646	48	100.0	114	2	US-09-248-796A-23116	Sequence 23116, A
574	48	100.0	77	2	US-09-643-597-361	Sequence 361, App	647	48	100.0	116	2	US-09-270-767-36280	Sequence 36280, A
575	48	100.0	77	2	US-09-630-940B-361	Sequence 361, App	648	48	100.0	116	2	US-09-270-767-51497	Sequence 51497, A
576	48	100.0	77	2	US-10-007-700-361	Sequence 361, App	649	48	100.0	117	2	US-09-622-613C-22	Sequence 22, Appl
577	48	100.0	78	2	US-09-248-796A-23216	Sequence 23216, App	650	48	100.0	117	2	US-09-581-894A-12	Sequence 12, Appl
578	48	100.0	78	2	US-09-248-796A-25811	Sequence 25811, A	651	48	100.0	118	2	US-09-084-303B-9	Sequence 9, Appl1
579	48	100.0	79	1	US-08-448-418-97	Sequence 97, Appl	652	48	100.0	118	2	US-09-205-658-120	Sequence 120, App
580	48	100.0	79	2	US-09-146-979-97	Sequence 97, Appl	653	48	100.0	118	2	US-09-581-894A-1	Sequence 1, Appl1
581	48	100.0	79	2	US-09-248-796A-27876	Sequence 27876, A	654	48	100.0	118	2	US-09-581-894A-10	Sequence 10, Appl
582	48	100.0	80	2	US-09-174-943-4	Sequence 4, Appl1	655	48	100.0	119	2	US-09-979-338A-32	Sequence 32, Appl
583	48	100.0	80	2	US-09-084-303B-15	Sequence 15, Appl	656	48	100.0	120	2	US-08-341-566B-2	Sequence 2, Appl1
584	48	100.0	80	2	US-09-248-796A-15929	Sequence 15929, A	657	48	100.0	120	2	US-08-353-944-2	Sequence 2, Appl1
585	48	100.0	81	1	US-08-717-169-15	Sequence 15, Appl	658	48	100.0	120	2	US-10-162-127-2	Sequence 2, Appl1
586	48	100.0	81	2	US-09-228-901A-15	Sequence 15, Appl	659	48	100.0	120	2	US-09-581-894A-2	Sequence 2, Appl1
587	48	100.0	82	2	US-09-979-338A-27	Sequence 27, Appl	660	48	100.0	120	4	PCR-US93-03895-2	Sequence 2, Appl1
588	48	100.0	84	2	US-09-270-767-57811	Sequence 57811, A	661	48	100.0	121	2	US-08-341-566B-4	Sequence 4, Appl1
589	48	100.0	85	2	US-08-772-440-32	Sequence 32, Appl	662	48	100.0	121	2	US-08-353-944-12	Sequence 12, Appl
590	48	100.0	85	2	US-09-256-976-82	Sequence 82, Appl	663	48	100.0	121	2	US-09-613-303-12	Sequence 12, Appl
591	48	100.0	85	2	US-09-280-030-65	Sequence 65, Appl	664	48	100.0	121	2	US-10-162-127-4	Sequence 4, Appl1
592	48	100.0	87	1	US-08-160-670A-7	Sequence 7, Appl1	665	48	100.0	121	2	US-10-267-311-12	Sequence 12, Appl
593	48	100.0	89	1	US-08-340-812-13	Sequence 13, Appl	666	48	100.0	121	2	US-08-931-855B-16	Sequence 16, Appl
594	48	100.0	89	1	US-08-459-064B-13	Sequence 13, Appl	667	48	100.0	121	2	US-09-581-894A-3	Sequence 3, Appl1
595	48	100.0	89	1	US-08-460-421A-13	Sequence 13, Appl	668	48	100.0	121	4	PCR-US93-03895-4	Sequence 4, Appl1
596	48	100.0	89	1	US-08-717-169-7	Sequence 7, Appl1	669	48	100.0	122	2	US-08-956-307B-19	Sequence 19, Appl
597	48	100.0	89	2	US-09-507-323B-12	Sequence 12, Appl	670	48	100.0	122	2	US-09-270-767-42087	Sequence 42087, A
598	48	100.0	89	2	US-09-228-901A-7	Sequence 7, Appl1	671	48	100.0	124	1	US-08-434-705B-16	Sequence 16, Appl
599	48	100.0	89	2	US-09-545-894-29	Sequence 29, Appl	672	48	100.0	124	1	US-09-086-620-16	Sequence 16, Appl
600	48	100.0	90	2	US-09-175-713-12	Sequence 12, Appl	673	48	100.0	124	2	US-09-042-071-39	Sequence 39, Appl
601	48	100.0	91	2	US-09-509-391-16	Sequence 16, Appl	674	48	100.0	124	2	US-09-09-042-071-39	Sequence 39, Appl
602	48	100.0	91	2	US-10-148-306-18	Sequence 18, Appl	675	48	100.0	126	1	US-08-268-346A-12	Sequence 12, Appl
603	48	100.0	92	2	US-09-979-338A-31	Sequence 31, Appl	676	48	100.0	127	2	US-08-467-023-188	Sequence 188, App
604	48	100.0	93	2	US-09-248-796A-24094	Sequence 24094, A	677	48	100.0	127	2	US-08-467-023-189	Sequence 189, App
605	48	100.0	93	2	US-09-509-391-17	Sequence 17, Appl	678	48	100.0	127	2	US-08-467-023-190	Sequence 190, App
606	48	100.0	94	2	US-09-256-976-95	Sequence 95, Appl	679	48	100.0	127	2	US-09-481-620A-8	Sequence 40, Appl
607	48	100.0	94	2	US-09-556-877-89	Sequence 89, Appl	680	48	100.0	127	2	US-09-481-620A-72	Sequence 72, Appl
608	48	100.0	94	2	US-09-620-412C-89	Sequence 89, Appl	681	48	100.0	128	2	US-08-467-023-187	Sequence 187, App
609	48	100.0	94	2	US-09-410-568-89	Sequence 89, Appl	682	48	100.0	128	2	US-09-012-097A-42	Sequence 22, Appl
610	48	100.0	94	2	US-09-598-419-89	Sequence 89, Appl	683	48	100.0	128	2	US-09-742-373-9	Sequence 9, Appl1
611	48	100.0	94	2	US-09-175-713-13	Sequence 13, Appl	684	48	100.0	128	2	US-09-781-804-21	Sequence 21, Appl

665	48	100.0	128	2	US-10-394-058-9	Sequence 9, Appl1	758	48	100.0	166	2	US-10-012-896-838	Sequence 838, App
666	48	100.0	129	2	US-09-556-877-91	Sequence 91, Appl1	759	48	100.0	166	2	US-10-089-019-10	Sequence 10, Appl1
667	48	100.0	129	2	US-09-620-412C-91	Sequence 91, Appl1	760	48	100.0	167	2	US-09-507-323B-13	Sequence 13, Appl1
668	48	100.0	129	2	US-09-410-568-91	Sequence 91, Appl1	761	48	100.0	167	2	US-09-741-243C-4	Sequence 4, Appl1
669	48	100.0	129	2	US-09-598-419-91	Sequence 91, Appl1	762	48	100.0	167	2	US-09-675-923-8	Sequence 8, Appl1
680	48	100.0	130	2	US-09-280-030-62	Sequence 62, Appl1	763	48	100.0	167	2	US-10-017-754-1921	Sequence 1921, Ap
681	48	100.0	130	2	US-09-270-767-35206	Sequence 35206, A	764	48	100.0	167	2	US-09-563-760A-30	Sequence 30, Appl1
682	48	100.0	130	2	US-09-370-767-54423	Sequence 54423, A	765	48	100.0	167	2	US-09-798-338B-10	Sequence 27, Appl1
683	48	100.0	131	2	US-09-367-309A-2	Sequence 2, Appl1	766	48	100.0	168	2	US-09-468-647A-27	Sequence 27, Appl1
684	48	100.0	132	2	US-09-771-161A-158	Sequence 158, App	767	48	100.0	168	2	US-09-468-647A-126	Sequence 126, App
685	48	100.0	133	1	US-08-268-348A-8	Sequence 8, Appl1	768	48	100.0	170	2	US-09-896-580B-6	Sequence 6, Appl1
686	48	100.0	133	1	US-08-268-348A-10	Sequence 10, Appl1	769	48	100.0	170	2	US-10-068-059-4	Sequence 4, Appl1
687	48	100.0	133	1	US-09-556-877-304	Sequence 304, App	770	48	100.0	171	2	US-09-646-028-9	Sequence 9, Appl1
688	48	100.0	133	2	US-09-620-412C-304	Sequence 304, App	771	48	100.0	172	2	US-08-860-165-12	Sequence 12, Appl1
689	48	100.0	133	2	US-09-598-419-304	Sequence 304, App	772	48	100.0	172	2	US-08-860-165-14	Sequence 14, Appl1
700	48	100.0	139	2	US-08-856-253-8	Sequence 8, Appl1	773	48	100.0	172	2	US-09-359-382-12	Sequence 12, Appl1
701	48	100.0	140	2	US-09-280-030-64	Sequence 64, Appl1	774	48	100.0	172	2	US-09-359-382-14	Sequence 14, Appl1
702	48	100.0	140	2	US-09-645-415A-60	Sequence 60, Appl1	775	48	100.0	175	2	US-09-248-796A-16887	Sequence 16887, A
703	48	100.0	143	2	US-09-674-183-16	Sequence 16, Appl1	776	48	100.0	177	2	US-09-058-483-4	Sequence 4, Appl1
704	48	100.0	144	2	US-09-330-421-3	Sequence 3, Appl1	777	48	100.0	177	2	US-09-695-437A-59	Sequence 59, Appl1
705	48	100.0	145	2	US-09-640-211A-794	Sequence 794, App	778	48	100.0	178	2	US-09-042-071-42	Sequence 42, Appl1
706	48	100.0	146	2	US-09-554-765-11	Sequence 11, Appl1	779	48	100.0	178	2	US-09-183-841-2	Sequence 2, Appl1
707	48	100.0	146	2	US-09-923-304-9	Sequence 9, Appl1	780	48	100.0	178	2	US-09-409-096-8	Sequence 8, Appl1
708	48	100.0	147	2	US-08-122-458D-9	Sequence 9, Appl1	781	48	100.0	178	2	US-09-813-718-6	Sequence 6, Appl1
709	48	100.0	147	2	US-09-554-765-10	Sequence 10, Appl1	782	48	100.0	180	2	US-08-772-440-31	Sequence 31, Appl1
710	48	100.0	148	2	US-09-828-523A-94	Sequence 94, Appl1	783	48	100.0	180	2	US-09-230-078A-4	Sequence 4, Appl1
711	48	100.0	149	2	US-09-646-028-6	Sequence 6, Appl1	784	48	100.0	183	2	US-09-832-659A-4	Sequence 4, Appl1
712	48	100.0	149	2	US-09-270-767-38212	Sequence 38212, A	785	48	100.0	183	2	US-09-832-658A-2	Sequence 2, Appl1
713	48	100.0	149	2	US-09-270-767-53429	Sequence 53429, A	786	48	100.0	184	2	US-09-023-082A-10	Sequence 30, Appl1
714	48	100.0	149	2	US-09-468-647A-124	Sequence 124, App	787	48	100.0	184	2	US-09-248-998-30	Sequence 30, Appl1
715	48	100.0	151	2	US-09-646-028-7	Sequence 7, Appl1	788	48	100.0	184	2	US-09-610-651-30	Sequence 30, Appl1
716	48	100.0	151	2	US-09-646-028-8	Sequence 8, Appl1	789	48	100.0	184	2	US-09-248-796A-24480	Sequence 24480, A
717	48	100.0	152	2	US-09-927-738-22	Sequence 22, Appl1	790	48	100.0	184	2	US-09-921-144-20	Sequence 20, Appl1
718	48	100.0	153	2	US-09-675-922-2	Sequence 2, Appl1	791	48	100.0	184	2	US-09-345-373-30	Sequence 30, Appl1
719	48	100.0	153	2	US-09-563-760B-32	Sequence 32, Appl1	792	48	100.0	184	2	US-10-075-446-30	Sequence 30, Appl1
720	48	100.0	153	2	US-09-798-338B-14	Sequence 14, Appl1	793	48	100.0	185	2	US-09-058-493-18	Sequence 18, Appl1
721	48	100.0	155	2	US-10-237-551-181	Sequence 181, App	794	48	100.0	185	2	US-09-921-144-18	Sequence 18, Appl1
722	48	100.0	156	2	US-09-270-767-40443	Sequence 40443, A	795	48	100.0	186	2	US-09-270-767-38819	Sequence 38819, A
723	48	100.0	156	2	US-09-270-767-55659	Sequence 55659, A	796	48	100.0	186	2	US-09-270-767-54036	Sequence 54036, A
724	48	100.0	156	2	US-09-586-937-69	Sequence 69, Appl1	797	48	100.0	188	2	US-09-828-523A-58	Sequence 58, Appl1
725	48	100.0	157	2	US-08-875-533-46	Sequence 46, Appl1	798	48	100.0	191	2	US-09-561-500-13	Sequence 13, Appl1
726	48	100.0	157	2	US-09-675-922-4	Sequence 4, Appl1	799	48	100.0	191	2	US-09-561-528-13	Sequence 13, Appl1
727	48	100.0	157	2	US-09-563-760A-34	Sequence 34, Appl1	800	48	100.0	191	2	US-09-561-528-13	Sequence 13, Appl1
728	48	100.0	157	2	US-09-798-338B-16	Sequence 16, Appl1	801	48	100.0	191	2	US-09-561-499-13	Sequence 13, Appl1
729	48	100.0	158	2	US-08-875-533-47	Sequence 47, Appl1	802	48	100.0	191	2	US-09-998-831-13	Sequence 13, Appl1
730	48	100.0	159	2	US-08-991-890-4	Sequence 4, Appl1	803	48	100.0	191	2	US-09-561-005-13	Sequence 13, Appl1
731	48	100.0	159	2	US-08-856-253-2	Sequence 2, Appl1	804	48	100.0	191	2	US-09-562-245-13	Sequence 13, Appl1
732	48	100.0	159	2	US-09-166-966E-8	Sequence 8, Appl1	805	48	100.0	191	2	US-10-148-306-19	Sequence 19, Appl1
733	48	100.0	159	2	US-09-518-842-4	Sequence 4, Appl1	806	48	100.0	192	2	US-09-771-161A-159	Sequence 159, App
734	48	100.0	160	2	US-09-355-700-59	Sequence 59, Appl1	807	48	100.0	193	2	US-09-874-923-119	Sequence 119, App
735	48	100.0	160	2	US-09-534-376A-59	Sequence 59, Appl1	808	48	100.0	195	2	US-09-042-071-40	Sequence 40, Appl1
736	48	100.0	160	2	US-10-089-019-18	Sequence 18, App	809	48	100.0	195	2	US-08-849-634B-3	Sequence 3, Appl1
737	48	100.0	161	2	US-09-636-215-846	Sequence 846, App	810	48	100.0	195	2	US-09-546-04-5	Sequence 5, Appl1
738	48	100.0	161	2	US-09-685-166A-846	Sequence 846, App	811	48	100.0	197	2	US-09-248-796A-23752	Sequence 23752, A
739	48	100.0	161	2	US-09-679-426-846	Sequence 846, App	812	48	100.0	198	1	US-08-642-253-111	Sequence 111, App
740	48	100.0	161	2	US-09-159-143-846	Sequence 846, App	813	48	100.0	198	1	US-08-397-633A-41	Sequence 41, Appl1
741	48	100.0	161	2	US-09-651-236-846	Sequence 846, App	814	48	100.0	198	1	US-08-397-633A-52	Sequence 52, Appl1
742	48	100.0	161	2	US-09-657-279-846	Sequence 846, App	815	48	100.0	198	2	US-09-248-796A-17554	Sequence 17554, A
743	48	100.0	161	2	US-10-012-896-846	Sequence 846, App	816	48	100.0	201	2	US-09-695-437A-61	Sequence 61, Appl1
744	48	100.0	161	2	US-10-007-700-423	Sequence 423, App	817	48	100.0	202	2	US-09-556-877-92	Sequence 92, Appl1
745	48	100.0	162	2	US-09-921-144-16	Sequence 16, Appl1	818	48	100.0	202	2	US-09-620-412C-92	Sequence 92, Appl1
746	48	100.0	163	2	US-09-675-922-6	Sequence 6, Appl1	819	48	100.0	202	2	US-09-410-568-92	Sequence 92, Appl1
747	48	100.0	163	2	US-09-248-796A-22113	Sequence 22113, A	820	48	100.0	202	2	US-09-598-419-92	Sequence 92, Appl1
748	48	100.0	163	2	US-09-921-144-14	Sequence 14, Appl1	821	48	100.0	203	2	US-09-270-767-35326	Sequence 35326, A
749	48	100.0	163	2	US-09-563-760A-24	Sequence 24, Appl1	822	48	100.0	203	2	US-09-270-767-350543	Sequence 350543, A
750	48	100.0	163	2	US-09-798-338B-18	Sequence 18, Appl1	823	48	100.0	206	2	US-09-183-861-26	Sequence 26, Appl1
751	48	100.0	166	2	US-09-646-028-5	Sequence 5, Appl1	824	48	100.0	206	2	US-09-022-765-26	Sequence 26, Appl1
752	48	100.0	166	2	US-09-636-215-838	Sequence 838, App	825	48	100.0	206	2	US-09-551-974A-26	Sequence 26, Appl1
753	48	100.0	166	2	US-09-685-166A-838	Sequence 838, App	826	48	100.0	206	2	US-09-565-501A-26	Sequence 26, Appl1
754	48	100.0	166	2	US-09-679-426-838	Sequence 838, App	827	48	100.0	206	2	US-09-639-206A-26	Sequence 26, Appl1
755	48	100.0	166	2	US-09-759-143-838	Sequence 838, App	828	48	100.0	206	2	US-09-874-923-26	Sequence 26, Appl1
756	48	100.0	166	2	US-09-651-236-838	Sequence 838, App	829	48	100.0	206	2	US-09-270-767-55211	Sequence 55211, A
757	48	100.0	166	2	US-09-657-279-838	Sequence 838, App	830	48	100.0	206	2	US-08-798-841-26	Sequence 26, Appl1

831	48	100.0	207	2	US-09-702-705-1667	Sequence 1667, Ap	904	48	100.0	225	2	US-09-456-090A-98	Sequence 98, Appl
832	48	100.0	207	2	US-09-736-457-1667	Sequence 1667, Ap	905	48	100.0	225	2	US-09-456-090A-100	Sequence 100, App
833	48	100.0	207	2	US-09-614-1248-1667	Sequence 1667, Ap	906	48	100.0	225	2	US-09-456-090A-102	Sequence 102, App
834	48	100.0	207	2	US-09-671-325-1667	Sequence 1667, Ap	907	48	100.0	225	2	US-09-456-090A-106	Sequence 106, App
835	48	100.0	207	2	US-09-658-824-1667	Sequence 1667, Ap	908	48	100.0	225	2	US-09-456-090A-108	Sequence 108, App
836	48	100.0	207	2	US-10-017-754-1667	Sequence 1667, Ap	909	48	100.0	225	2	US-09-456-090A-110	Sequence 110, App
837	48	100.0	207	2	US-10-017-754-1913	Sequence 1913, Ap	910	48	100.0	225	2	US-09-453-234-54	Sequence 54, Appl
838	48	100.0	207	2	US-09-651-563-1667	Sequence 1667, Ap	911	48	100.0	225	2	US-09-453-234-56	Sequence 56, Appl
839	48	100.0	207	2	US-09-771-161A-160	Sequence 160, App	912	48	100.0	225	2	US-09-453-234-60	Sequence 60, Appl
840	48	100.0	209	2	US-09-166-966E-11	Sequence 11, Appl	913	48	100.0	225	2	US-09-453-234-62	Sequence 62, Appl
841	48	100.0	210	1	US-08-234-783-2	Sequence 2, Appl	914	48	100.0	225	2	US-09-453-234-66	Sequence 66, Appl
842	48	100.0	210	1	US-08-456-907-2	Sequence 28, Appl	915	48	100.0	225	2	US-09-453-234-68	Sequence 68, Appl
843	48	100.0	210	1	US-08-612-973-28	Sequence 28, Appl	916	48	100.0	225	2	US-09-453-234-66	Sequence 66, Appl
844	48	100.0	210	2	US-08-927-597-28	Sequence 28, Appl	917	48	100.0	225	2	US-09-453-234-70	Sequence 70, Appl
845	48	100.0	210	2	US-08-928-757-28	Sequence 28, Appl	918	48	100.0	225	2	US-09-453-234-92	Sequence 92, Appl
846	48	100.0	210	4	PCT-US95-05523-2	Sequence 2, Appl	919	48	100.0	225	2	US-09-453-234-94	Sequence 94, Appl
847	48	100.0	211	2	US-08-856-253-4	Sequence 46, Appl	920	48	100.0	225	2	US-09-453-234-96	Sequence 96, Appl
848	48	100.0	211	2	US-09-612-314A-46	Sequence 46, Appl	921	48	100.0	225	2	US-09-453-234-98	Sequence 98, Appl
849	48	100.0	214	2	US-09-632-553-1	Sequence 1, Appl	922	48	100.0	225	2	US-09-453-234-100	Sequence 100, App
850	48	100.0	214	2	US-09-963-156A-1	Sequence 1, Appl	923	48	100.0	225	2	US-09-453-234-102	Sequence 102, App
851	48	100.0	215	2	US-09-198-723A-46	Sequence 46, Appl	924	48	100.0	225	2	US-09-453-234-106	Sequence 106, App
852	48	100.0	215	2	US-09-198-723A-50	Sequence 50, Appl	925	48	100.0	225	2	US-09-453-234-108	Sequence 108, App
853	48	100.0	215	2	US-09-198-723A-53	Sequence 53, Appl	926	48	100.0	225	2	US-09-453-234-110	Sequence 110, App
854	48	100.0	215	2	US-09-198-723A-57	Sequence 57, Appl	927	48	100.0	226	2	US-08-865-468-1	Sequence 1, Appl
855	48	100.0	215	2	US-09-684-881-46	Sequence 46, Appl	928	48	100.0	226	2	US-08-898-649-1	Sequence 1, Appl
856	48	100.0	215	2	US-09-684-881-50	Sequence 50, Appl	929	48	100.0	227	2	US-09-485-885-16	Sequence 16, Appl
857	48	100.0	215	2	US-09-684-881-53	Sequence 53, Appl	930	48	100.0	227	2	US-09-485-885-19	Sequence 19, Appl
858	48	100.0	215	2	US-09-684-881-57	Sequence 57, Appl	931	48	100.0	228	2	US-09-248-796A-15127	Sequence 15127, A
859	48	100.0	215	2	US-09-949-016-6554	Sequence 6554, Ap	932	48	100.0	229	2	US-09-546-043-8	Sequence 8, Appl
860	48	100.0	216	2	US-09-198-723A-1	Sequence 1, Appl	933	48	100.0	230	2	US-09-485-737B-102	Sequence 102, Appl
861	48	100.0	216	2	US-09-198-723A-2	Sequence 2, Appl	934	48	100.0	230	2	US-09-248-796A-21362	Sequence 21362, A
862	48	100.0	216	2	US-09-198-723A-3	Sequence 3, Appl	935	48	100.0	230	2	US-10-071-486A-102	Sequence 102, App
863	48	100.0	216	2	US-09-198-723A-4	Sequence 4, Appl	936	48	100.0	231	2	US-09-287-849-28	Sequence 28, Appl
864	48	100.0	216	2	US-09-198-723A-5	Sequence 5, Appl	937	48	100.0	231	2	US-09-324-258-20	Sequence 20, Appl
865	48	100.0	216	2	US-09-198-723A-6	Sequence 6, Appl	938	48	100.0	233	1	US-08-480-753-2	Sequence 2, Appl
866	48	100.0	216	2	US-09-198-723A-7	Sequence 7, Appl	939	48	100.0	233	2	US-09-041-889-9	Sequence 9, Appl
867	48	100.0	216	2	US-09-198-723A-8	Sequence 8, Appl	940	48	100.0	233	2	US-08-837-058-9	Sequence 9, Appl
868	48	100.0	216	2	US-09-198-723A-9	Sequence 9, Appl	941	48	100.0	233	2	US-09-417-264-9	Sequence 9, Appl
869	48	100.0	216	2	US-09-198-723A-10	Sequence 10, Appl	942	48	100.0	233	2	US-09-324-258-16	Sequence 16, Appl
870	48	100.0	216	2	US-09-684-881-1	Sequence 1, Appl	943	48	100.0	234	2	US-09-009-217-2	Sequence 2, Appl
871	48	100.0	216	2	US-09-684-881-2	Sequence 2, Appl	944	48	100.0	234	2	US-09-009-217-3	Sequence 3, Appl
872	48	100.0	216	2	US-09-684-881-3	Sequence 3, Appl	945	48	100.0	234	2	US-09-009-656-2	Sequence 2, Appl
873	48	100.0	216	2	US-09-684-881-4	Sequence 4, Appl	946	48	100.0	234	2	US-09-009-656-3	Sequence 3, Appl
874	48	100.0	216	2	US-09-684-881-5	Sequence 5, Appl	947	48	100.0	235	2	US-09-009-217-6	Sequence 6, Appl
875	48	100.0	216	2	US-09-684-881-6	Sequence 6, Appl	948	48	100.0	235	2	US-09-009-656-6	Sequence 6, Appl
876	48	100.0	216	2	US-09-684-881-7	Sequence 7, Appl	949	48	100.0	235	2	US-09-009-656-5	Sequence 5, Appl
877	48	100.0	216	2	US-09-684-881-8	Sequence 8, Appl	950	48	100.0	235	2	US-10-071-485-93	Sequence 93, Appl
878	48	100.0	216	2	US-09-684-881-9	Sequence 9, Appl	951	48	100.0	236	2	US-09-009-217-7	Sequence 7, Appl
879	48	100.0	216	2	US-09-684-881-10	Sequence 10, Appl	952	48	100.0	236	2	US-09-009-656-7	Sequence 7, Appl
880	48	100.0	218	2	US-09-674-183-14	Sequence 14, Appl	953	48	100.0	236	2	US-09-456-090A-64	Sequence 64, Appl
881	48	100.0	219	1	US-08-621-081A-16	Sequence 16, Appl	954	48	100.0	236	2	US-09-456-090A-104	Sequence 104, App
882	48	100.0	220	2	US-09-485-885-1	Sequence 1, Appl	955	48	100.0	236	2	US-09-453-234-64	Sequence 64, Appl
883	48	100.0	220	2	US-09-485-885-8	Sequence 8, Appl	956	48	100.0	236	2	US-09-453-234-104	Sequence 104, App
884	48	100.0	220	2	US-09-270-767-61056	Sequence 61056, A	957	48	100.0	236	2	US-10-358-790-2	Sequence 2, Appl
885	48	100.0	221	1	US-08-621-081A-19	Sequence 19, Appl	958	48	100.0	238	2	US-10-197-220-112	Sequence 124, App
886	48	100.0	224	2	US-09-636-215-825	Sequence 825, App	959	48	100.0	239	2	US-09-485-885-12	Sequence 124, App
887	48	100.0	224	2	US-09-685-166A-825	Sequence 825, App	960	48	100.0	240	2	US-09-485-737B-91	Sequence 91, Appl
888	48	100.0	224	2	US-09-679-426-825	Sequence 825, App	961	48	100.0	240	2	US-09-435-054A-10	Sequence 10, Appl
889	48	100.0	224	2	US-09-759-143-825	Sequence 825, App	962	48	100.0	240	2	US-10-071-485-91	Sequence 91, Appl
890	48	100.0	224	2	US-09-651-236-825	Sequence 825, App	963	48	100.0	241	2	US-09-651-236-842	Sequence 842, App
891	48	100.0	224	2	US-09-657-279-825	Sequence 825, App	964	48	100.0	241	2	US-09-657-279-842	Sequence 842, App
892	48	100.0	224	2	US-10-012-896-825	Sequence 825, App	965	48	100.0	241	2	US-10-012-896-842	Sequence 842, App
893	48	100.0	225	2	US-09-456-090A-54	Sequence 54, Appl	966	48	100.0	241	2	US-09-679-426-842	Sequence 842, App
894	48	100.0	225	2	US-09-456-090A-56	Sequence 56, Appl	967	48	100.0	241	2	US-09-759-143-842	Sequence 842, App
895	48	100.0	225	2	US-09-456-090A-58	Sequence 58, Appl	968	48	100.0	241	2	US-09-651-236-842	Sequence 842, App
896	48	100.0	225	2	US-09-456-090A-60	Sequence 60, Appl	969	48	100.0	241	2	US-09-657-279-842	Sequence 842, App
897	48	100.0	225	2	US-09-456-090A-62	Sequence 62, Appl	970	48	100.0	242	2	US-10-012-896-842	Sequence 842, App
898	48	100.0	225	2	US-09-456-090A-66	Sequence 66, Appl	971	48	100.0	242	2	US-09-167-434-8	Sequence 8, Appl
899	48	100.0	225	2	US-09-456-090A-68	Sequence 68, Appl	972	48	100.0	242	2	US-08-853-755-8	Sequence 9, Appl
900	48	100.0	225	2	US-09-456-090A-70	Sequence 70, Appl	973	48	100.0	243	2	US-09-167-434-9	Sequence 9, Appl
901	48	100.0	225	2	US-09-456-090A-92	Sequence 92, Appl	974	48	100.0	243	2	US-08-853-755-9	Sequence 9, Appl
902	48	100.0	225	2	US-09-456-090A-94	Sequence 94, Appl	975	48	100.0	243	2	US-09-828-523A-50	Sequence 50, Appl
903	48	100.0	225	2	US-09-456-090A-96	Sequence 96, Appl	976	48	100.0	244	1	US-08-480-755-4	Sequence 4, Appl

977 48 100.0 246 2 US-09-167-434-11 Sequence 11, Appl
978 48 100.0 246 2 US-08-853-755-11 Sequence 11, Appl
979 48 100.0 246 2 US-09-546-043-6 Sequence 6, Appl
980 48 100.0 246 2 US-09-248-796A-16241 Sequence 16241, A
981 48 100.0 248 2 US-08-341-560B-8 Sequence 8, Appl
982 48 100.0 248 2 US-08-353-940-8 Sequence 8, Appl
983 48 100.0 248 2 US-09-649-063-23 Sequence 23, Appl
984 48 100.0 248 2 US-10-162-127-8 Sequence 8, Appl
985 48 100.0 248 4 PCT-US93-03895-8 Sequence 8, Appl
986 48 100.0 249 1 US-08-155-171B-32 Sequence 32, Appl
987 48 100.0 249 1 US-08-435-998-32 Sequence 32, Appl
988 48 100.0 249 2 US-09-324-258-17 Sequence 17, Appl
989 48 100.0 250 2 US-08-341-560B-6 Sequence 6, Appl
990 48 100.0 250 2 US-08-353-940-6 Sequence 6, Appl
991 48 100.0 250 2 US-10-162-127-6 Sequence 6, Appl
992 48 100.0 250 1 PCT-US93-03895-6 Sequence 6, Appl
993 48 100.0 251 1 US-08-397-633A-74 Sequence 74, Appl
994 48 100.0 253 2 US-09-270-767-42427 Sequence 42427, A
995 48 100.0 254 1 US-08-792-824-4 Sequence 4, Appl
996 48 100.0 254 1 US-08-792-824-7 Sequence 7, Appl
997 48 100.0 254 1 US-08-792-824-10 Sequence 10, Appl
998 48 100.0 254 1 US-08-792-824-13 Sequence 13, Appl
999 48 100.0 254 2 US-09-167-434-7 Sequence 7, Appl
1000 48 100.0 254 2 US-08-853-755-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-160-670A-6
; Sequence 6, Application US/08160670A
; Patent No. 5449758
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Protein Size Marker Ladder
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,670A
; FILING DATE: 12/2/93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bismond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.2580000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-08-160-670A-6

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||

Db 1 HHHHHH 6

RESULT 2
US-08-140-222-1
; Sequence 1, Application US/08140222
; Patent No. 5470952
; GENERAL INFORMATION:
; APPLICANT: Stahl, et al.
; TITLE OF INVENTION: CNF Family Antagonists
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/140,222
; FILING DATE: 20-OCT-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempner Ph.D., Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-347-2113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-140-222-1

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||

Db 1 HHHHHH 6

RESULT 3
US-08-131-365B-48
; Sequence 48, Application US/08131365B
; Patent No. 5527690
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Briggs, Michael R.
; APPLICANT: Wang, Xiaodong
; APPLICANT: Goldstein, Joseph L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
; TO STEROL AND STEROL REGULATORY ELEMENT BINDING
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77210
; COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/131,365B
FILING DATE: 01-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-131-365B-48

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 4
US-08-469-486-47
Sequence 47, Application US/08469486
Patent No. 5739281
GENERAL INFORMATION:
APPLICANT: Thoegeersen, Hans Christian
APPLICANT: Holter, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flern & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-469-486-47

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 5
US-08-460-343B-51
Sequence 51, Application US/08460343B
Patent No. 5741664
GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,343B
FILING DATE: 01-Jun-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398028
FILING DATE: 03-mar-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kuflinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8228
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-460-343B-51

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 6
US-08-299-567-1
Sequence 1, Application US/08299567
Patent No. 5747033
GENERAL INFORMATION:

APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF BPH FAMILY LIGANDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kempster, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-299-567-1

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 7
US-08-398-028B-51
Sequence 51, Application US/08398028B
Patent No. 5780285
GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,028B
FILING DATE: 03-Mar-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kudinec, Jeffrey S.
REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0936
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8228
TELEFAX: 650/952-9891
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-028B-51

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 8
US-08-660-626-4
Sequence 4, Application US/08660626
Patent No. 5789655
GENERAL INFORMATION:
APPLICANT: Stanley B. Prusiner
APPLICANT: Glenn C. Telling
APPLICANT: Fred B. Cohen
APPLICANT: Michael R. Scott
TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
TITLE OF INVENTION: EPTIPE-TAGGED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,626
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Valeta Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 07532/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-626-4

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 9

US-08-434-705B-17
; Sequence 17, Application US/08434705B
; Patent No. 5798258
; GENERAL INFORMATION:
; APPLICANT: Douglas Ph.D., James
; TITLE OF INVENTION: CART PROTEIN AND DNA ENCODING THEREFOR
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis K. Shelton
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,705B
; FILING DATE: May 4, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: OHSU18446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-8100
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-434-705B-17

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 10
US-08-470-837-22
; Sequence 22, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimmi, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 1150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-837-22

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 11
US-08-472-244-14
; Sequence 14, Application US/08472244
; Patent No. 5821088
; GENERAL INFORMATION:
; APPLICANT: Darzins, Aldis
; APPLICANT: Whitehead, Stephen
; APPLICANT: Hruby, Dennis E.
; TITLE OF INVENTION: Use of Gram-Positive Bacteria to Express
; TITLE OF INVENTION: Recombinant Proteins
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,244
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 016921-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-472-244-14

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
11111
DB 1 HHHHH 6

RESULT 12

US-08-504-265B-51
Sequence 51, Application US/08504265B
Patent No. 5837516
GENERAL INFORMATION:
APPLICANT: Marcue D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,265B
FILING DATE: 19-Jul-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398028
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8228
TELEFAX: 650/952-9881
INFORMATION FOR SEQ. ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-504-265B-51

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
11111
DB 1 HHHHH 6

RESULT 13

US-08-623-833B-16
Sequence 16, Application US/08623833B
Patent No. 5866683

GENERAL INFORMATION:
APPLICANT: SHIMURA, Kiyohito
APPLICANT: KASAI, Kenichi
APPLICANT: MATSUMOTO, Hiroyuki
APPLICANT: TAKAMOTO, Hisayoshi
TITLE OF INVENTION: ISOELECTRIC POINT MARKERS FOR
NUMBER OF SEQUENCES: 69
TITLE OF INVENTION: ISOELECTRIC FOCUSING WITH FLUORESCENCE DETECTION
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,833B
FILING DATE: 29-MAR-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 076863/1995
FILING DATE: 31-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 271196/1995
FILING DATE: 19-OCT-1995
INFORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acid
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-623-833B-16

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
11111
DB 1 HHHHH 6

RESULT 14

US-08-652-507-8
Sequence 8, Application US/08652507
Patent No. 5876691

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vandertye, P.C.
STREET: 1100 No. 5876691th Glebe Road, 8th floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILING DATE: 02-Jul-1996
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-211
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-507-8

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
1 HHHHH 6

RESULT 15
US-08-668-123-48
Sequence 48, Application US/08668123
Patent No. 5891631

GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TO STEROL REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,123
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/131,365
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.

REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-668-123-48

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
1 HHHHH 6

RESULT 16
US-08-469-658-47

Sequence 47, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Th egeresen, Hans Christian
APPLICANT: Holter, Thor Laa

APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REPRODING OF
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version

SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-469-658-47

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
1 HHHHH 6

RESULT 17
US-09-086-201-17

Sequence 17, Application US/09086201
Patent No. 5969103
GENERAL INFORMATION:
APPLICANT: Douglas Ph. D., James

TITLE OF INVENTION: CART PROTEIN AND DNA ENCODING THEREFOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis K. Shelton
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,201
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,705
FILING DATE: May 4, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: OHSU18446
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-09-086-201-17

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
DB 1 HHHHHH 6

RESULT 18
US-08-591-196-57
Sequence 57, Application US/08591196
Patent No. 5977316
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,196
FILING DATE: 16-JAN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-591-196-57

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
DB 1 HHHHHH 6

RESULT 19
US-08-996-139-18
Sequence 18, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-18

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
DB 1 HHHHHH 6

RESULT 20
US-08-481-435-42
; Sequence 42, Application US/08481435
; Patent No. 6027906
; GENERAL INFORMATION:
; APPLICANT: Baiganesh, Tanjore S
; APPLICANT: Town, Christine
; TITLE OF INVENTION: No. 6027906el Polypeptides
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,435
; FILING DATE: 10-JUL-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IN 580/MMS/94
; FILING DATE: 01-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9404072-2
; FILING DATE: 24-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 354-8113
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-435-42

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 21
US-08-772-440-28
; Sequence 28, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Arizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2, COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas

COUNTRY: USA
ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-772-440-28

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 22
US-09-267-031-18
; Sequence 18, Application US/09267031
; Patent No. 6137031
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yuelin
; APPLICANT: Kinkema, Mark
; APPLICANT: Dong, Xinlian
; APPLICANT: Ronald, Pamela
; APPLICANT: Chern, Mawsheng
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: DNA Binding Proteins That Interact With NPRI
; FILE REFERENCE: 023070-092500US
; CURRENT APPLICATION NUMBER: US/09/267,031
; CURRENT FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: (His)6-tag
; US-09-267-031-18

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 23
US-09-398-341-1
; Sequence 1, Application US/09398341

Patent No. 6146842
GENERAL INFORMATION:
APPLICANT: Josiah, Serene
APPLICANT: Boischalt, Michael
TITLE OF INVENTION: High-Throughput Screening Assays Utilizing Metal-
TITLE OF INVENTION: Chelate Capture
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: ONE POST OFFICE SQUARE
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,341
FILING DATE: 17-SEP-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-116.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-398-341-1

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 24
US-09-031-168-4
Sequence 4, Application US/09031168
Patent No. 6150583
GENERAL INFORMATION:
APPLICANT: Stanley B. Prusiner
APPLICANT: Glenn C. Telling
APPLICANT: Fred E. Cohen
APPLICANT: Michael R. Scott
TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
TITLE OF INVENTION: EPIPOPE-TAGGED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascliti
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,168

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,626
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Valecia Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 07532/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-031-168-4

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 25
US-08-789-333F-99
Sequence 99, Application US/08789333F
Patent No. 6153380
GENERAL INFORMATION:
APPLICANT: Rothenberg, S. M.
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
FILE REFERENCE: A642601DJBMSDS
CURRENT APPLICATION NUMBER: US/08/789,333F
CURRENT FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: 08/589,108
PRIOR FILING DATE: 1996-01-23
PRIOR APPLICATION NUMBER: 08/589,911
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 99
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: histidine tag
US-08-789-333F-99

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 26
US-08-995-659-18
Sequence 18, Application US/0895659
Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Marabkovsky, Eugene

```

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; APPLICATION NUMBER: USN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-995-659-18

Query Match          100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 27
; Sequence 26, Application US/09142334
; Patent No. 6268485
; GENERAL INFORMATION:
; APPLICANT: Faries, Timothy C.
; APPLICANT: Harrison, Richard A.
; TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
; FILE REFERENCE: 4-30443/A/IRU/PCT
; CURRENT APPLICATION NUMBER: US/09/142,334
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: PCT/GB97/00603
; EARLIER FILING DATE: 1997-03-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: insertion
; US-09-142-334-26

Query Match          100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 28
; US-09-215-649A-18
; Sequence 18, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,649A
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
; US-09-215-649A-18

Query Match          100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 29
```

US-09-140-084-7
; Sequence 7, Application US/09140084A
; Patent No. 630065
; GENERAL INFORMATION:
; APPLICANT: Kieke, et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
; FILE REFERENCE: D6061CIP2
; CURRENT APPLICATION NUMBER: US/09/140,084A
; CURRENT FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Epitope Tag
US-09-140-084-7

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 30
US-09-382-950-4
; Sequence 4, Application US/09382950
; Patent No. 6303337
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Kenneth
; APPLICANT: Gite, Sadanand
; APPLICANT: Olejnik, Jerzy
; TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Proteins
; FILE REFERENCE: AMBER-03879
; CURRENT APPLICATION NUMBER: US/09/382,950
; CURRENT FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: ().()
; OTHER INFORMATION: Synthetic
US-09-382-950-4

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 31
US-09-382-736B-5
; Sequence 5, Application US/09382736B
; Patent No. 6306628
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Kenneth
; APPLICANT: Gite, Sadanand
; APPLICANT: Olejnik, Jerzy
; TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Pro
; FILE REFERENCE: AMBER-03951
; CURRENT APPLICATION NUMBER: US/09/382,736B
; CURRENT FILING DATE: 1999-08-25

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-382-736B-5

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 32
US-08-977-378-2
; Sequence 2, Application US/08977378
; Patent No. 6309842
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Gates, Christopher M.
; Heinkel, Gregory L.
; Lalonde, Guy
; Matheakis, Larry C.
; Paddon, Christopher J.
; Schatz, Peter J.
; TITLE OF INVENTION: Use of Modified Tethers in Screening
; Compound Libraries
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,378
; FILING DATE: 24-No. 6309842-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,307
; FILING DATE: 03-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16528A-018010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-977-378-2

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 33
US-09-353-555-2
; Sequence 2, Application US/09353555
; Patent No. 6329209
; GENERAL INFORMATION:
; APPLICANT: Wagner, Peter
; APPLICANT: No. 6329209K, Steffen
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Irlin, Christian
; TITLE OF INVENTION: Arrays of Protein-Capture Agents and Methods of Use
; FILE REFERENCE: 24406-0006
; CURRENT APPLICATION NUMBER: US/09/353,555
; CURRENT FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: US 09/115,455
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: histidine tag
US-09-353-555-2

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 34
US-08-868-452-22
; Sequence 22, Application US/08868452C
; Patent No. 6352972
; GENERAL INFORMATION:
; APPLICANT: Marcel E. Nimmi
; APPLICANT: Frederick L. Hall
; APPLICANT: Lingtao Wu
; APPLICANT: Bo Han
; APPLICANT: Edwin Shors
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEINS AND THEIR
; FILE REFERENCE: 17972-11
; CURRENT APPLICATION NUMBER: US/08/868,452C
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatsSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Human
US-08-868-452-22

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 35
US-09-000-094-47
; Sequence 47, Application US/09000094
; Patent No. 6365160
; GENERAL INFORMATION:
; APPLICANT: WEBB, Elizabeth Ann
; MARGERTS, Mary Brigid
; COX, John Cooper
; FRAZER, Ian
; MCWILLIAN, Nigel Alan John
; WILLIAMS, Mark Philip
; MOJONEY, Margaret Bridget
; Holland
; EDWARDS, Scirling John

; TITLE OF INVENTION: PAPILLOMAVIRUS POLYPEPTIDE CONSTRUCTS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESS: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/000,094
; FILING DATE: 21-Apr-1998
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU96/00473
; FILING DATE: 26-JUL-1996
; APPLICATION NUMBER: AU PN 4439/95
; FILING DATE: 27-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 017227/0137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-000-094-47

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 36
US-09-058-483-7
; Sequence 7, Application US/09058483A
; Patent No. 6365347
; GENERAL INFORMATION:
; APPLICANT: Murray, Andrew W.
; APPLICANT: Smith, Dana L.
; APPLICANT: Sorger, Peter K.
; APPLICANT: No. 6365347man, Thea C.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING DISRUPTORS OF BIOLOGICAL

;; TITLE OF INVENTION: PATHWAYS USING GENETIC SELECTION
;; FILE REFERENCE: 30432.1US11
;; CURRENT APPLICATION NUMBER: US/09/058,483A
;; CURRENT FILING DATE: 1998-04-10
;; EARLIER APPLICATION NUMBER: 08/835,727
;; EARLIER FILING DATE: 1997-04-11
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO: 7
;; LENGTH: 6
;; TYPE: PR1
;; ORGANISM: amino acid sequence of Staphylococcus aureus nuclease protei
US-09-058-483-7

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 37
US-09-140-201-8
; Sequence 8, Application US/09140201
; Patent No. 6372425
; GENERAL INFORMATION:
; APPLICANT: KELLER, P.
; TITLE OF INVENTION: LARGE SCALE AFFINITY CHROMATOGRAPHY OF
; TITLE OF INVENTION: MACROMOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACK TRIBBLE
; STREET: P. O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/140,201
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/329,749
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: TRIBBLE, JACK
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: 18780
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-140-201-8

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |

Db 1 HHHHHH 6

RESULT 38
US-09-039-780A-106
; Sequence 106, Application US/09039780A
; Patent No. 6376248
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NELSON, PAMELA
; LAN, JIANQING
; SHIH, POJEN
; JESSE, JOEL A.
; SCHIFFERLI, KEVIN P.
; GEBREYERHU, GULIAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREENLEAF, WINNER & SULLIVAN
; STREET: 5370 MANHATTAN CIRCLE, SUITE 201
; CITY: BOULDER
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,780A
; FILING DATE: 16-Mar-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SULLIVAN, SALLY A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 32-95C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-09-039-780A-106

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 39
US-09-291-170A-14
; Sequence 14, Application US/09291170A
; Patent No. 6410687
; GENERAL INFORMATION:
; APPLICANT: Vale, Ronald D.
; APPLICANT: Hartman, James J.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Assays for the Detection of Microtubule
; FILE REFERENCE: 185578-000510US
; CURRENT APPLICATION NUMBER: US/09/291,170A
; CURRENT FILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: US 60/081,734
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: (His)6 or 6xHis
US-09-291-170A-14

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 40
US-09-577-780-18
Sequence 18, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-577-780-18

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 41
US-09-724-297-7
Sequence 7, Application US/09724297
Patent No. 642538
GENERAL INFORMATION:
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: Wiltrop, et al.
TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
FILE REFERENCE: 97-99C
CURRENT APPLICATION NUMBER: US/09/724,297
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/009,388
PRIOR FILING DATE: 1998-01-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 6
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: misc.feature
LOCATION: ().()
OTHER INFORMATION: Epitope tag
US-09-724-297-7

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 42
US-09-367-309A-4
Sequence 4, Application US/09367309A
Patent No. 6428807
GENERAL INFORMATION:
APPLICANT: MACFARLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: 6-His tag
US-09-367-309A-4

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 43

US-09-724-884-14
; Sequence 14, Application US/09724884
; Patent No. 6429304

GENERAL INFORMATION:

APPLICANT: Vale, Ronald D.
APPLICANT: Hartman, James J.

TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Assays for the Detection of Microtubule

FILE REFERENCE: 18557B-00051005
CURRENT APPLICATION NUMBER: US/09/724,884

PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/291,170

PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14

LENGTH: 6
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: (His)6 or 6xHis
US-09-724-884-14

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

US-09-529-279-6

RESULT 44

US-09-529-279-6
; Sequence 6, Application US/09529279
; Patent No. 6451617

GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO
APPLICANT: OHTOMO, TOSHIHIKO

APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

FILE REFERENCE: 053466/0278
CURRENT APPLICATION NUMBER: US/09/529,279

PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: PCT/JP98/04796

PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: JP 9/290188

PRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6

LENGTH: 6
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-529-279-6

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 45

US-09-313-942-1
; Sequence 1, Application US/09313942
; Patent No. 6472179

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942

PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1

LENGTH: 6
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Tag sequence
US-09-313-942-1

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

US-09-353-215-6
; Sequence 6, Application US/09353215
; Patent No. 6475808

GENERAL INFORMATION:

APPLICANT: Wagner, Peter
APPLICANT: Ault-Riche, Dana

APPLICANT: No. 6475808k, Steffen
TITLE OF INVENTION: Itcin, Christian

FILE REFERENCE: 24406-0004P1
CURRENT APPLICATION NUMBER: US/09/353,215

PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/115,455

PRIOR FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6

LENGTH: 6
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: histidine tag
US-09-353-215-6

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

US-09-577-800-18
; Sequence 18, Application US/09577800
; Patent No. 6479635

RESULT 47
US-09-577-800-18
; Sequence 18, Application US/09577800
; Patent No. 6479635

```
/
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, Dirk M.
/ APPLICANT: Galibert, Laurent
/ APPLICANT: Maraskovsky, Eugene
/ TITLE OF INVENTION: Receptor Activator of NF-kappaB
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Immunex Corporation, Law Department
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Power Macintosh
/ OPERATING SYSTEM: Apple Operating System 7.5.5
/ SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/577,800
/ FILING DATE: 24-MAY-2000
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/996,139
/ FILING DATE: 22 DECEMBER 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 60/064,671
/ FILING DATE: 14 OCTOBER 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/813,509
/ FILING DATE: 07 MARCH 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/772,330
/ FILING DATE: 23 DECEMBER 1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,693
/ REFERENCE/DOCKET NUMBER: 2851-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)233-0644
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-09-577-800-18
/
/ Query Match          100.0%; Score 48; DB 2; Length 6;
/ Best Local Similarity 100.0%; Pred. No. 4.6e+05;
/ Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 HHHHHH 6
/      |||||
/ Db 1 HHHHHH 6
/
/ RESULT 48
/ US-09-667-422-7
/ Sequence 7, Application US/09667422
/ Patent No. 6482611
/ GENERAL INFORMATION:
/ APPLICANT: Cortright, Daniel
/ APPLICANT: Krause, James
/ TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
/ FILE REFERENCE: HCR
/ CURRENT APPLICATION NUMBER: US/09/667,422
/ CURRENT FILING DATE: 2001-06-07
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 7
/ LENGTH: 6
```

```
/
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:His6x epitope
/
/ US-09-667-422-7
/
/ Query Match          100.0%; Score 48; DB 2; Length 6;
/ Best Local Similarity 100.0%; Pred. No. 4.6e+05;
/ Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 HHHHHH 6
/      |||||
/ Db 1 HHHHHH 6
/
/ RESULT 49
/ US-09-315-926A-81
/ Sequence 81, Application US/09315926A
/ Patent No. 6498027
/ GENERAL INFORMATION:
/ APPLICANT: Es van, Helmut
/ APPLICANT: Havenga, Menzo
/ APPLICANT: Verlinden, Stefan
/ TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
/ FILE REFERENCE: 2183-4080US
/ CURRENT APPLICATION NUMBER: US/09/315,926A
/ CURRENT FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: EP 99201593.3
/ PRIOR FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: EP 98201693.3
/ PRIOR FILING DATE: 1998-05-20
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO-81
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: Description of Artificial Sequence: phage
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(6)
/ OTHER INFORMATION: /note="hCAT1 amino acid sequence"
/
/ US-09-315-926A-81
/
/ Query Match          100.0%; Score 48; DB 2; Length 6;
/ Best Local Similarity 100.0%; Pred. No. 4.6e+05;
/ Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 HHHHHH 6
/      |||||
/ Db 1 HHHHHH 6
/
/ RESULT 50
/ US-09-731-558-11
/ Sequence 11, Application US/09731558
/ Patent No. 6503717
/ GENERAL INFORMATION:
/ APPLICANT: Case, Casey Christopher
/ APPLICANT: Liu, Qiang
/ APPLICANT: Rebar, Edward J.
/ APPLICANT: Sangamo Biosciences, Inc.
/ TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
/ PROTEINS OF INVENTION: Proteins for the Identification of Gene Function
/ FILE REFERENCE: 019496-003210US
/ CURRENT APPLICATION NUMBER: US/09/731,558
/ CURRENT FILING DATE: 2000-12-06
/ PRIOR APPLICATION NUMBER: US 09/456,100
/ PRIOR FILING DATE: 1999-12-06
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 11
```

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:6xHis tag
US-09-731-558-11

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||
Db 1 HHHHHH 6

Search completed: March 21, 2006, 11:09:39
Job time : 55 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:09:01 ; Search time 165 Seconds
(without alignments)
15.194 Million cell updates/sec

Title: US-10-719-523-5
Perfect score: 48
Sequence: 1 HHHHHH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA.Main:*
1: /cgn2_6/prodata/1/pubppaa/us07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppaa/us08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppaa/us09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppaa/us10a_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppaa/us10b_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppaa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	6	3	US-09-280-030-61
2	48	100.0	6	3	US-09-771-956-11
3	48	100.0	6	3	US-09-822-485-30
4	48	100.0	6	3	US-09-760-008A-9
5	48	100.0	6	3	US-09-728-911-12
6	48	100.0	6	3	US-09-313-942-1
7	48	100.0	6	3	US-09-809-517A-11
8	48	100.0	6	3	US-09-211-691-14
9	48	100.0	6	3	US-09-808-037-33
10	48	100.0	6	3	US-09-888-615-149
11	48	100.0	6	3	US-09-875-519A-26
12	48	100.0	6	3	US-09-367-309A-4
13	48	100.0	6	3	US-09-837-992-44
14	48	100.0	6	3	US-09-871-856-18
15	48	100.0	6	3	US-09-801-968-22
16	48	100.0	6	3	US-09-865-363-18
17	48	100.0	6	3	US-09-871-291-18
18	48	100.0	6	3	US-09-875-338-93
19	48	100.0	6	3	US-09-988-899-5
20	48	100.0	6	3	US-09-798-884-16
21	48	100.0	6	3	US-09-817-764-9
22	48	100.0	6	3	US-09-943-382-1
23	48	100.0	6	3	US-09-951-265-2
24	48	100.0	6	3	US-09-801-676A-2
25	48	100.0	6	3	US-09-916-940-99
26	48	100.0	6	3	US-09-780-933-14
27	48	100.0	6	3	US-09-900-530A-15

28	48	100.0	6	3	US-09-973-145-4	Sequence 4, Appl1
29	48	100.0	6	3	US-09-731-558-11	Sequence 11, Appl1
30	48	100.0	6	3	US-09-822-698A-22	Sequence 22, Appl1
31	48	100.0	6	3	US-09-144-886-5	Sequence 5, Appl1
32	48	100.0	6	3	US-09-935-868-1	Sequence 1, Appl1
33	48	100.0	6	3	US-09-877-650-18	Sequence 18, Appl1
34	48	100.0	6	3	US-09-814-604-9	Sequence 9, Appl1
35	48	100.0	6	3	US-09-939-769-94	Sequence 94, Appl1
36	48	100.0	6	3	US-09-935-430-698	Sequence 698, Appl1
37	48	100.0	6	3	US-09-821-726-19	Sequence 19, Appl1
38	48	100.0	6	3	US-09-945-248B-3	Sequence 3, Appl1
39	48	100.0	6	3	US-09-997-623-41	Sequence 41, Appl1
40	48	100.0	6	3	US-09-978-917A-41	Sequence 41, Appl1
41	48	100.0	6	3	US-09-948-391A-43	Sequence 43, Appl1
42	48	100.0	6	3	US-09-989-981A-11	Sequence 11, Appl1
43	48	100.0	6	3	US-09-904-196B-9	Sequence 9, Appl1
44	48	100.0	6	3	US-09-911-569-106	Sequence 106, Appl1
45	48	100.0	6	3	US-09-922-226-43	Sequence 43, Appl1
46	48	100.0	6	3	US-09-906-311C-15	Sequence 15, Appl1
47	48	100.0	6	3	US-09-782-587B-12	Sequence 12, Appl1
48	48	100.0	6	3	US-09-802-154-22	Sequence 22, Appl1
49	48	100.0	6	3	US-09-961-400-43	Sequence 43, Appl1
50	48	100.0	6	3	US-09-932-165-1480	Sequence 1480, Appl1
51	48	100.0	6	3	US-09-834-597-32	Sequence 32, Appl1
52	48	100.0	6	3	US-09-874-907A-2	Sequence 2, Appl1
53	48	100.0	6	3	US-09-925-055D-13	Sequence 13, Appl1
54	48	100.0	6	3	US-09-870-353A-30	Sequence 30, Appl1
55	48	100.0	6	3	US-09-949-039-4	Sequence 4, Appl1
56	48	100.0	6	3	US-09-935-384-780	Sequence 780, Appl1
57	48	100.0	6	3	US-09-942-052-709	Sequence 709, Appl1
58	48	100.0	6	3	US-09-962-745-11778	Sequence 1778, Appl1
59	48	100.0	6	3	US-09-807-742-12	Sequence 12, Appl1
60	48	100.0	6	3	US-09-784-553C-61	Sequence 61, Appl1
61	48	100.0	6	3	US-09-796-076-1	Sequence 1, Appl1
62	48	100.0	6	3	US-09-813-197-5	Sequence 5, Appl1
63	48	100.0	6	4	US-10-046-442-2	Sequence 2, Appl1
64	48	100.0	6	4	US-10-003-496-9	Sequence 9, Appl1
65	48	100.0	6	4	US-10-005-646-16	Sequence 16, Appl1
66	48	100.0	6	4	US-10-158-895-6	Sequence 6, Appl1
67	48	100.0	6	4	US-10-029-009-17	Sequence 17, Appl1
68	48	100.0	6	4	US-10-093-200A-10	Sequence 10, Appl1
69	48	100.0	6	4	US-10-116-273-35	Sequence 35, Appl1
70	48	100.0	6	4	US-10-061-395-68	Sequence 68, Appl1
71	48	100.0	6	4	US-10-147-087-6	Sequence 6, Appl1
72	48	100.0	6	4	US-10-151-071-6	Sequence 6, Appl1
73	48	100.0	6	4	US-10-166-232A-6	Sequence 6, Appl1
74	48	100.0	6	4	US-10-083-815-1	Sequence 1, Appl1
75	48	100.0	6	4	US-10-077-023-93	Sequence 93, Appl1
76	48	100.0	6	4	US-10-015-979-12	Sequence 12, Appl1
77	48	100.0	6	4	US-10-071-838-13	Sequence 13, Appl1
78	48	100.0	6	4	US-10-058-636-6	Sequence 6, Appl1
79	48	100.0	6	4	US-10-035-045-24	Sequence 24, Appl1
80	48	100.0	6	4	US-10-092-934-11	Sequence 11, Appl1
81	48	100.0	6	4	US-10-047-991-12	Sequence 12, Appl1
82	48	100.0	6	4	US-10-090-365-12	Sequence 12, Appl1
83	48	100.0	6	4	US-10-059-261-286	Sequence 286, Appl1
84	48	100.0	6	4	US-10-059-271-80	Sequence 80, Appl1
85	48	100.0	6	4	US-10-001-469-1402	Sequence 1402, Appl1
86	48	100.0	6	4	US-10-259-460-2	Sequence 2, Appl1
87	48	100.0	6	4	US-10-174-368A-4	Sequence 4, Appl1
88	48	100.0	6	4	US-10-222-952A-13	Sequence 13, Appl1
89	48	100.0	6	4	US-10-093-248-10	Sequence 10, Appl1
90	48	100.0	6	4	US-10-119-235-2	Sequence 2, Appl1
91	48	100.0	6	4	US-10-104-919-12	Sequence 12, Appl1
92	48	100.0	6	4	US-10-153-882-10	Sequence 10, Appl1
93	48	100.0	6	4	US-10-287-035-1	Sequence 1, Appl1
94	48	100.0	6	4	US-10-128-590-63	Sequence 63, Appl1
95	48	100.0	6	4	US-10-322-142-17	Sequence 17, Appl1
96	48	100.0	6	4	US-10-370-071-2	Sequence 2, Appl1
97	48	100.0	6	4	US-10-134-643-25	Sequence 25, Appl1
98	48	100.0	6	4	US-10-309-515-3	Sequence 3, Appl1
99	48	100.0	6	4	US-10-192-294-9	Sequence 9, Appl1
100	48	100.0	6	4	US-10-195-707B-35	Sequence 35, Appl1

101	48	100.0	6	4	US-10-037-243-46	Sequence 46, App1	174	48	100.0	6	4	US-10-058-270A-139	Sequence 139, App
102	48	100.0	6	4	US-10-032-214-299	Sequence 299, App	175	48	100.0	6	4	US-10-449-831A-164	Sequence 164, App
103	48	100.0	6	4	US-10-066-965A-9	Sequence 9, App1	176	48	100.0	6	4	US-10-211-462-230	Sequence 230, App
104	48	100.0	6	4	US-10-282-162-1	Sequence 1, App1	177	48	100.0	6	4	US-10-668-778-5	Sequence 5, App1
105	48	100.0	6	4	US-10-200-879-106	Sequence 106, App	178	48	100.0	6	4	US-10-667-494-43	Sequence 43, App1
106	48	100.0	6	4	US-10-256-705-13	Sequence 13, App1	179	48	100.0	6	4	US-10-181-937-78	Sequence 78, App1
107	48	100.0	6	4	US-10-342-103-9	Sequence 9, App1	180	48	100.0	6	4	US-10-147-299A-33	Sequence 33, App1
108	48	100.0	6	4	US-10-270-073-20	Sequence 20, App1	181	48	100.0	6	4	US-10-253-286-357	Sequence 357, App
109	48	100.0	6	4	US-10-291-990-13	Sequence .13, App1	182	48	100.0	6	4	US-10-275-107-71	Sequence 71, App1
110	48	100.0	6	4	US-10-315-964A-40	Sequence 400, App	183	48	100.0	6	4	US-10-459-199-23	Sequence 23, App1
111	48	100.0	6	4	US-10-317-251A-400	Sequence 400, App	184	48	100.0	6	4	US-10-339-744-6	Sequence 6, App1
112	48	100.0	6	4	US-10-317-252A-400	Sequence 400, App	185	48	100.0	6	4	US-10-188-832-207	Sequence 207, App
113	48	100.0	6	4	US-10-021-660-135	Sequence 135, App	186	48	100.0	6	4	US-10-280-133-17	Sequence 17, App1
114	48	100.0	6	4	US-10-128-587A-63	Sequence 63, App1	187	48	100.0	6	4	US-10-667-462-43	Sequence 43, App1
115	48	100.0	6	4	US-10-340-860A-41	Sequence 41, App1	188	48	100.0	6	4	US-10-667-464-43	Sequence 43, App1
116	48	100.0	6	4	US-10-227-617A-6	Sequence 6, App1	189	48	100.0	6	4	US-10-644-055-1	Sequence 1, App1
117	48	100.0	6	4	US-10-168-080-22	Sequence 22, App1	190	48	100.0	6	4	US-10-665-227-3	Sequence 3, App1
118	48	100.0	6	4	US-10-318-966-9	Sequence 9, App1	191	48	100.0	6	4	US-10-627-473-42	Sequence 42, App1
119	48	100.0	6	4	US-10-181-804A-13	Sequence 13, App1	192	48	100.0	6	4	US-10-691-383-20	Sequence 20, App1
120	48	100.0	6	4	US-10-384-743-6	Sequence 6, App1	193	48	100.0	6	4	US-10-372-966-9	Sequence 9, App1
121	48	100.0	6	4	US-10-328-190-16	Sequence 16, App1	194	48	100.0	6	4	US-10-676-299-13	Sequence 13, App1
122	48	100.0	6	4	US-10-190-414-16	Sequence 16, App1	195	48	100.0	6	4	US-10-676-296-13	Sequence 13, App1
123	48	100.0	6	4	US-10-235-175-81	Sequence 81, App1	196	48	100.0	6	4	US-10-662-906-2	Sequence 2, App1
124	48	100.0	6	4	US-10-126-764-3	Sequence 3, App1	197	48	100.0	6	4	US-10-626-905-53	Sequence 53, App1
125	48	100.0	6	4	US-10-084-706-49	Sequence 49, App1	198	48	100.0	6	4	US-10-363-552-76	Sequence 76, App1
126	48	100.0	6	4	US-10-374-207-30	Sequence 30, App1	199	48	100.0	6	4	US-10-612-410-20	Sequence 20, App1
127	48	100.0	6	4	US-10-325-720-39	Sequence 39, App1	200	48	100.0	6	4	US-10-656-624-4	Sequence 4, App1
128	48	100.0	6	4	US-10-351-189-39	Sequence 39, App1	201	48	100.0	6	4	US-10-467-243-27	Sequence 27, App1
129	48	100.0	6	4	US-10-405-878A-18	Sequence 18, App1	202	48	100.0	6	4	US-10-441-779C-21	Sequence 21, App1
130	48	100.0	6	4	US-10-325-717-72	Sequence 72, App1	203	48	100.0	6	4	US-10-628-432-23	Sequence 23, App1
131	48	100.0	6	4	US-10-321-558-4	Sequence 4, App1	204	48	100.0	6	4	US-10-664-421-167	Sequence 167, App
132	48	100.0	6	4	US-10-317-773-14	Sequence 14, App1	205	48	100.0	6	4	US-10-346-658-1	Sequence 1, App1
133	48	100.0	6	4	US-10-203-531-3	Sequence 3, App1	206	48	100.0	6	4	US-10-738-454-7	Sequence 7, App1
134	48	100.0	6	4	US-10-317-428-14	Sequence 14, App1	207	48	100.0	6	4	US-10-799-016-6	Sequence 6, App1
135	48	100.0	6	4	US-10-321-204-53	Sequence 53, App1	208	48	100.0	6	4	US-10-344-607-1	Sequence 1, App1
136	48	100.0	6	4	US-10-264-127-5	Sequence 5, App1	209	48	100.0	6	4	US-10-761-781-14	Sequence 14, App1
137	48	100.0	6	4	US-10-277-292-698	Sequence 698, App1	210	48	100.0	6	4	US-10-159-257A-207	Sequence 207, App
138	48	100.0	6	4	US-10-168-447-22	Sequence 22, App1	211	48	100.0	6	4	US-10-651-674-7	Sequence 7, App1
139	48	100.0	6	4	US-10-167-634-66	Sequence 66, App1	212	48	100.0	6	4	US-10-377-268-34	Sequence 34, App1
140	48	100.0	6	4	US-10-280-340-698	Sequence 698, App	213	48	100.0	6	4	US-10-701-919-11	Sequence 11, App1
141	48	100.0	6	4	US-10-187-967-1	Sequence 1, App1	214	48	100.0	6	4	US-10-472-724-20	Sequence 20, App1
142	48	100.0	6	4	US-10-292-088-145	Sequence 145, App	215	48	100.0	6	4	US-10-693-057-358	Sequence 358, App
143	48	100.0	6	4	US-10-128-578B-63	Sequence 63, App1	216	48	100.0	6	4	US-10-821-274-2	Sequence 2, App1
144	48	100.0	6	4	US-10-417-924A-3	Sequence 3, App1	217	48	100.0	6	4	US-10-821-583-30	Sequence 30, App1
145	48	100.0	6	4	US-10-336-840-39	Sequence 39, App1	218	48	100.0	6	4	US-10-699-550-20	Sequence 20, App1
146	48	100.0	6	4	US-10-366-493-101	Sequence 101, App	219	48	100.0	6	4	US-10-618-941-138	Sequence 138, App
147	48	100.0	6	4	US-10-273-180-30	Sequence 30, App1	220	48	100.0	6	4	US-10-409-814A-19	Sequence 19, App1
148	48	100.0	6	4	US-10-013-312-2990	Sequence 2990, App	221	48	100.0	6	4	US-10-725-276-24	Sequence 24, App1
149	48	100.0	6	4	US-10-256-851-7	Sequence 7, App1	222	48	100.0	6	4	US-10-677-641-10	Sequence 10, App1
150	48	100.0	6	4	US-10-045-674-12	Sequence 12, App1	223	48	100.0	6	4	US-10-627-592-38	Sequence 38, App1
151	48	100.0	6	4	US-10-295-027-1382	Sequence 1382, App	224	48	100.0	6	4	US-10-768-976-20	Sequence 20, App1
152	48	100.0	6	4	US-10-245-871-357	Sequence 357, App	225	48	100.0	6	5	US-10-622-088-50	Sequence 50, App1
153	48	100.0	6	4	US-10-175-689-32	Sequence 32, App1	226	48	100.0	6	5	US-10-470-987-17	Sequence 17, App1
154	48	100.0	6	4	US-10-253-471-1778	Sequence 1778, App	227	48	100.0	6	5	US-10-627-582-47	Sequence 47, App1
155	48	100.0	6	4	US-10-336-041A-4	Sequence 4, App1	228	48	100.0	6	5	US-10-706-328-1	Sequence 1, App1
156	48	100.0	6	4	US-10-057-475B-10979	Sequence 10979, A	229	48	100.0	6	5	US-10-810-262-33	Sequence 33, App1
157	48	100.0	6	4	US-10-422-523-23	Sequence 23, App1	230	48	100.0	6	5	US-10-759-762-1	Sequence 1, App1
158	48	100.0	6	4	US-10-277-216-32	Sequence 32, App1	231	48	100.0	6	5	US-10-705-745-9	Sequence 9, App1
159	48	100.0	6	4	US-10-452-786-1	Sequence 1, App1	232	48	100.0	6	5	US-10-416-456A-30	Sequence 30, App1
160	48	100.0	6	4	US-10-173-999-161	Sequence 161, App	233	48	100.0	6	5	US-10-131-998A-42	Sequence 42, App1
161	48	100.0	6	4	US-10-374-726-52	Sequence 52, App1	234	48	100.0	6	5	US-10-627-649-286	Sequence 286, App
162	48	100.0	6	4	US-10-387-355-2	Sequence 2, App1	235	48	100.0	6	5	US-10-475-706-5	Sequence 5, App1
163	48	100.0	6	4	US-10-423-847-43	Sequence 43, App1	236	48	100.0	6	5	US-10-786-505-54	Sequence 54, App1
164	48	100.0	6	4	US-10-355-218-7	Sequence 7, App1	237	48	100.0	6	5	US-10-802-133-18	Sequence 18, App1
165	48	100.0	6	4	US-10-609-296-49	Sequence 49, App1	238	48	100.0	6	5	US-10-829-388-20	Sequence 20, App1
166	48	100.0	6	4	US-10-384-788-33	Sequence 33, App1	239	48	100.0	6	5	US-10-769-308-16	Sequence 16, App1
167	48	100.0	6	4	US-10-339-712-5	Sequence 5, App1	240	48	100.0	6	5	US-10-859-739-16	Sequence 16, App1
168	48	100.0	6	4	US-10-339-712-61	Sequence 61, App1	241	48	100.0	6	5	US-10-883-472-9	Sequence 9, App1
169	48	100.0	6	4	US-10-373-238-5	Sequence 5, App1	242	48	100.0	6	5	US-10-863-729-14	Sequence 14, App1
170	48	100.0	6	4	US-10-385-415-91	Sequence 91, App1	243	48	100.0	6	5	US-10-622-893A-15	Sequence 15, App1
171	48	100.0	6	4	US-10-444-691-5	Sequence 5, App1	244	48	100.0	6	5	US-10-884-783-3	Sequence 3, App1
172	48	100.0	6	4	US-10-126-022-32	Sequence 32, App1	245	48	100.0	6	5	US-10-926-225-11	Sequence 11, App1
173	48	100.0	6	4	US-10-253-493-1778	Sequence 1778, App	246	48	100.0	6	5	US-10-865-146-34	Sequence 34, App1

247	48	100.0	6	5	US-10-842-054-24	Sequence 24, Appl	320	48	100.0	6	5	US-10-839-793-1	Sequence 1, Appl1
248	48	100.0	6	5	US-10-946-786-3	Sequence 3, Appl1	321	48	100.0	6	5	US-10-503-050A-10	Sequence 10, Appl
249	48	100.0	6	5	US-10-842-989-16	Sequence 16, Appl	322	48	100.0	6	5	US-10-981-141-18	Sequence 18, Appl
250	48	100.0	6	5	US-10-719-523-5	Sequence 5, Appl1	323	48	100.0	6	5	US-10-994-824-93	Sequence 93, Appl
251	48	100.0	6	5	US-10-835-096-21	Sequence 21, Appl	324	48	100.0	6	5	US-10-982-543-1	Sequence 1, Appl1
252	48	100.0	6	5	US-10-725-284-24	Sequence 24, Appl	325	48	100.0	6	5	US-10-981-998-12	Sequence 12, Appl
253	48	100.0	6	5	US-10-857-673-19	Sequence 19, Appl	326	48	100.0	6	5	US-10-806-062-325	Sequence 325, App
254	48	100.0	6	5	US-10-754-485-49	Sequence 49, Appl	327	48	100.0	6	5	US-10-961-826-41	Sequence 41, Appl
255	48	100.0	6	5	US-10-831-063-43	Sequence 43, Appl	328	48	100.0	6	5	US-10-969-245-90	Sequence 90, Appl
256	48	100.0	6	5	US-10-854-735-28	Sequence 28, Appl	329	48	100.0	6	5	US-10-965-006-15	Sequence 15, Appl
257	48	100.0	6	5	US-10-839-615-4	Sequence 4, Appl1	330	48	100.0	6	5	US-10-756-813-16	Sequence 16, Appl
258	48	100.0	6	5	US-10-693-056-358	Sequence 358, App	331	48	100.0	6	5	US-10-971-736-474	Sequence 474, App
259	48	100.0	6	5	US-10-771-833-7	Sequence 7, Appl1	332	48	100.0	6	5	US-10-990-137-698	Sequence 698, App
260	48	100.0	6	5	US-10-843-951-54	Sequence 54, Appl	333	48	100.0	6	5	US-10-980-974-7	Sequence 7, Appl1
261	48	100.0	6	5	US-10-840-723-358	Sequence 358, App	334	48	100.0	6	5	US-10-804-687-63	Sequence 63, Appl
262	48	100.0	6	5	US-10-473-571-16	Sequence 16, Appl	335	48	100.0	6	5	US-10-971-606-5	Sequence 5, Appl1
263	48	100.0	6	5	US-10-497-003A-16	Sequence 16, Appl	336	48	100.0	6	6	US-11-004-111-41	Sequence 41, Appl
264	48	100.0	6	5	US-10-883-144-85	Sequence 85, Appl	337	48	100.0	6	6	US-11-004-461-9	Sequence 9, Appl1
265	48	100.0	6	5	US-10-661-366-12	Sequence 12, Appl	338	48	100.0	6	6	US-11-045-944-12	Sequence 12, Appl
266	48	100.0	6	5	US-10-628-004-28	Sequence 28, Appl	339	48	100.0	6	6	US-11-053-228-9	Sequence 9, Appl1
267	48	100.0	6	5	US-10-658-752-11	Sequence 11, Appl	340	48	100.0	6	6	US-11-093-103-110	Sequence 110, App
268	48	100.0	6	5	US-10-769-074-16	Sequence 16, Appl	341	48	100.0	6	6	US-11-112-137-10	Sequence 10, App
269	48	100.0	6	5	US-10-835-533-28	Sequence 28, Appl	342	48	100.0	6	6	US-11-115-906-35	Sequence 35, Appl
270	48	100.0	6	5	US-10-484-218-28	Sequence 28, Appl	343	48	100.0	6	6	US-11-035-623-40	Sequence 40, Appl
271	48	100.0	6	5	US-10-363-870A-11	Sequence 11, Appl	344	48	100.0	6	6	US-11-128-026-44	Sequence 44, Appl
272	48	100.0	6	5	US-10-899-551-50	Sequence 50, Appl	345	48	100.0	6	6	US-11-003-306-5	Sequence 5, Appl1
273	48	100.0	6	5	US-10-826-572-20	Sequence 20, Appl	346	48	100.0	6	6	US-11-029-242-11	Sequence 11, Appl
274	48	100.0	6	5	US-10-937-372-11	Sequence 11, Appl	347	48	100.0	6	6	US-11-134-114-1	Sequence 1, Appl1
275	48	100.0	6	5	US-10-968-432-12	Sequence 12, Appl	348	48	100.0	6	6	US-11-010-558-10	Sequence 10, Appl
276	48	100.0	6	5	US-10-473-524-16	Sequence 16, Appl	349	48	100.0	6	6	US-11-047-365-23	Sequence 23, Appl
277	48	100.0	6	5	US-10-897-387-72	Sequence 72, Appl	350	48	100.0	7	3	US-09-809-517A-12	Sequence 12, Appl
278	48	100.0	6	5	US-10-880-922-63	Sequence 63, Appl	351	48	100.0	7	3	US-09-809-517A-13	Sequence 13, Appl
279	48	100.0	6	5	US-10-886-949-7	Sequence 7, Appl1	352	48	100.0	7	3	US-09-963-761B-5	Sequence 5, Appl1
280	48	100.0	6	5	US-10-495-885-1	Sequence 1, Appl1	353	48	100.0	7	4	US-10-343-766-7	Sequence 7, Appl1
281	48	100.0	6	5	US-10-871-602-358	Sequence 358, App	354	48	100.0	7	4	US-10-665-227-3	Sequence 4, Appl1
282	48	100.0	6	5	US-10-944-496-17	Sequence 17, Appl	355	48	100.0	7	5	US-10-622-088-165	Sequence 165, App
283	48	100.0	6	5	US-10-805-684-161	Sequence 161, App	356	48	100.0	7	5	US-10-946-786-4	Sequence 4, Appl1
284	48	100.0	6	5	US-10-917-844-95	Sequence 95, Appl	357	48	100.0	7	5	US-10-658-752-12	Sequence 12, Appl
285	48	100.0	6	5	US-10-872-859-59	Sequence 59, Appl	358	48	100.0	7	5	US-10-658-752-13	Sequence 13, Appl
286	48	100.0	6	5	US-10-931-916-69	Sequence 69, Appl	359	48	100.0	7	5	US-10-501-071-9	Sequence 9, Appl1
287	48	100.0	6	5	US-10-966-097A-4	Sequence 4, Appl1	360	48	100.0	7	5	US-10-965-227-3	Sequence 3, Appl1
288	48	100.0	6	5	US-10-966-097A-18	Sequence 18, Appl	361	48	100.0	7	5	US-10-963-994-12	Sequence 12, Appl
289	48	100.0	6	5	US-10-703-817-254	Sequence 254, App	362	48	100.0	8	3	US-09-760-008A-11	Sequence 10, Appl
290	48	100.0	6	5	US-10-729-475-13	Sequence 13, Appl	363	48	100.0	8	3	US-09-334-477-11	Sequence 11, Appl
291	48	100.0	6	5	US-10-505-486-17	Sequence 17, Appl	364	48	100.0	8	3	US-09-244-984-2	Sequence 2, Appl1
292	48	100.0	6	5	US-10-984-958A-8	Sequence 8, Appl1	365	48	100.0	8	3	US-09-780-933-15	Sequence 15, Appl
293	48	100.0	6	5	US-10-922-339-43	Sequence 43, Appl	366	48	100.0	8	3	US-09-772-719-22	Sequence 22, Appl
294	48	100.0	6	5	US-10-501-071-8	Sequence 8, Appl1	367	48	100.0	8	3	US-09-997-623-42	Sequence 42, Appl
295	48	100.0	6	5	US-10-921-676-6	Sequence 6, Appl1	368	48	100.0	8	3	US-09-978-917A-42	Sequence 42, Appl
296	48	100.0	6	5	US-10-877-667A-6	Sequence 6, Appl1	369	48	100.0	8	3	US-09-967-237-22	Sequence 22, Appl
297	48	100.0	6	5	US-10-823-995-1	Sequence 1, Appl1	370	48	100.0	8	3	US-09-904-196B-10	Sequence 10, Appl
298	48	100.0	6	5	US-10-959-600-5	Sequence 5, Appl1	371	48	100.0	8	3	US-09-782-587B-13	Sequence 13, Appl
299	48	100.0	6	5	US-10-665-883-10	Sequence 10, Appl	372	48	100.0	8	4	US-10-003-496-10	Sequence 10, Appl
300	48	100.0	6	5	US-10-998-775-19	Sequence 19, Appl	373	48	100.0	8	4	US-10-116-273-36	Sequence 36, Appl
301	48	100.0	6	5	US-10-881-405-27	Sequence 27, Appl	374	48	100.0	8	4	US-10-057-321-2	Sequence 2, Appl1
302	48	100.0	6	5	US-10-957-433-2	Sequence 2, Appl1	375	48	100.0	8	4	US-10-156-634A-16	Sequence 16, Appl
303	48	100.0	6	5	US-10-479-901-299	Sequence 299, App	376	48	100.0	8	4	US-10-191-879-15	Sequence 15, Appl
304	48	100.0	6	5	US-10-820-474A-269	Sequence 269, App	377	48	100.0	8	4	US-10-194-728-5	Sequence 5, Appl1
305	48	100.0	6	5	US-10-871-369-13	Sequence 13, Appl	378	48	100.0	8	4	US-10-193-858-5	Sequence 5, Appl1
306	48	100.0	6	5	US-10-900-930-26	Sequence 26, Appl	379	48	100.0	8	4	US-10-192-294-10	Sequence 10, Appl
307	48	100.0	6	5	US-10-927-588-14	Sequence 14, Appl	380	48	100.0	8	4	US-10-195-707B-36	Sequence 36, Appl
308	48	100.0	6	5	US-10-941-635-167	Sequence 167, App	381	48	100.0	8	4	US-10-118-966-10	Sequence 10, Appl
309	48	100.0	6	5	US-10-971-679-358	Sequence 358, App	382	48	100.0	8	4	US-10-190-414-17	Sequence 17, Appl
310	48	100.0	6	5	US-10-764-212-81	Sequence 81, Appl	383	48	100.0	8	4	US-10-356-088-63	Sequence 63, Appl
311	48	100.0	6	5	US-10-872-770-13	Sequence 13, Appl	384	48	100.0	8	4	US-10-084-706-50	Sequence 50, Appl
312	48	100.0	6	5	US-10-903-476-13	Sequence 13, Appl	385	48	100.0	8	4	US-10-325-720-40	Sequence 40, Appl
313	48	100.0	6	5	US-10-965-227-4	Sequence 4, Appl1	386	48	100.0	8	4	US-10-351-189-40	Sequence 40, Appl
314	48	100.0	6	5	US-10-789-818-22	Sequence 22, Appl	387	48	100.0	8	4	US-10-325-717-73	Sequence 73, Appl
315	48	100.0	6	5	US-10-704-513-774	Sequence 774, App	388	48	100.0	8	4	US-10-303-531-4	Sequence 4, Appl1
316	48	100.0	6	5	US-10-805-075-9	Sequence 9, Appl1	389	48	100.0	8	4	US-10-366-493-102	Sequence 102, App
317	48	100.0	6	5	US-10-922-802-20	Sequence 20, Appl	390	48	100.0	8	4	US-10-609-296-50	Sequence 50, Appl
318	48	100.0	6	5	US-10-716-095A-14	Sequence 14, Appl	391	48	100.0	8	4	US-10-444-691-6	Sequence 6, Appl1
319	48	100.0	6	5	US-10-911-160-55	Sequence 55, Appl	392	48	100.0	8	4	US-10-351-891-120	Sequence 120, App

333	48	100.0	8	4	US-10-381-870-16	Sequence 16, Appl	466	48	100.0	10	2	US-08-464-363-73	Sequence 73, Appl
334	48	100.0	8	4	US-10-665-227-5	Sequence 5, Appl1	467	48	100.0	10	3	US-09-809-517A-2	Sequence 2, Appl1
335	48	100.0	8	4	US-10-296-733-16	Sequence 16, Appl	468	48	100.0	10	3	US-09-402-131-9	Sequence 9, Appl1
336	48	100.0	8	4	US-10-467-243-28	Sequence 28, Appl	469	48	100.0	10	3	US-09-981-636-2	Sequence 2, Appl1
337	48	100.0	8	4	US-10-741-204-36	Sequence 36, Appl	470	48	100.0	10	3	US-09-981-636-3	Sequence 3, Appl1
338	48	100.0	8	4	US-10-741-205-23	Sequence 23, Appl	471	48	100.0	10	3	US-09-911-568-101	Sequence 101, App
339	48	100.0	8	4	US-10-741-208-36	Sequence 36, Appl	472	48	100.0	10	3	US-09-976-935-31	Sequence 31, Appl
400	48	100.0	8	4	US-10-377-268-35	Sequence 35, Appl	473	48	100.0	10	3	US-09-933-780C-24	Sequence 24, Appl
401	48	100.0	8	4	US-10-799-326-63	Sequence 63, Appl	474	48	100.0	10	4	US-10-029-505-18	Sequence 18, Appl
402	48	100.0	8	5	US-10-699-113-25	Sequence 25, Appl	475	48	100.0	10	4	US-10-057-505-24	Sequence 24, Appl
403	48	100.0	8	5	US-10-705-743-10	Sequence 10, Appl	476	48	100.0	10	4	US-10-022-832-77	Sequence 77, Appl
404	48	100.0	8	5	US-10-795-933-22	Sequence 22, Appl	477	48	100.0	10	4	US-10-047-991-10	Sequence 10, Appl
405	48	100.0	8	5	US-10-784-300-2	Sequence 2, Appl1	478	48	100.0	10	4	US-10-174-410-6	Sequence 6, Appl1
406	48	100.0	8	5	US-10-888-694-22	Sequence 22, Appl1	479	48	100.0	10	4	US-10-174-410-11	Sequence 11, Appl
407	48	100.0	8	5	US-10-946-786-5	Sequence 5, Appl1	480	48	100.0	10	4	US-10-188-343-1	Sequence 1, Appl1
408	48	100.0	8	5	US-10-854-735-29	Sequence 29, Appl	481	48	100.0	10	4	US-10-104-919-60	Sequence 60, Appl
409	48	100.0	8	5	US-10-835-533-29	Sequence 29, Appl	482	48	100.0	10	4	US-10-286-421-7	Sequence 7, Appl1
410	48	100.0	8	5	US-10-898-616-10	Sequence 10, Appl	483	48	100.0	10	4	US-10-286-421-13	Sequence 13, Appl
411	48	100.0	8	5	US-10-612-358-7	Sequence 7, Appl1	484	48	100.0	10	4	US-10-200-879-101	Sequence 101, App
412	48	100.0	8	5	US-10-851-918B-17	Sequence 17, Appl	485	48	100.0	10	4	US-10-168-080-23	Sequence 23, Appl
413	48	100.0	8	5	US-10-851-918B-24	Sequence 24, Appl	486	48	100.0	10	4	US-10-291-851-7	Sequence 7, Appl1
414	48	100.0	8	5	US-10-851-918B-29	Sequence 29, Appl	487	48	100.0	10	4	US-10-181-804A-14	Sequence 14, Appl
415	48	100.0	8	5	US-10-851-918B-45	Sequence 45, Appl	488	48	100.0	10	4	US-10-291-190-58	Sequence 58, Appl
416	48	100.0	8	5	US-10-851-918B-50	Sequence 50, Appl	489	48	100.0	10	4	US-10-319-799-7	Sequence 7, Appl1
417	48	100.0	8	5	US-10-501-071-10	Sequence 10, Appl	490	48	100.0	10	4	US-10-319-799-13	Sequence 13, Appl
418	48	100.0	8	5	US-10-501-071-17	Sequence 17, Appl	491	48	100.0	10	4	US-10-306-762-6	Sequence 6, Appl1
419	48	100.0	8	5	US-10-756-813-17	Sequence 17, Appl	492	48	100.0	10	4	US-10-351-157-72	Sequence 72, Appl
420	48	100.0	8	5	US-10-980-597-3	Sequence 3, Appl1	493	48	100.0	10	4	US-10-408-167A-9	Sequence 9, Appl1
421	48	100.0	8	6	US-11-004-111-42	Sequence 42, Appl	494	48	100.0	10	4	US-10-352-554-72	Sequence 72, Appl
422	48	100.0	8	6	US-11-004-461-10	Sequence 10, Appl	495	48	100.0	10	4	US-10-385-415-78	Sequence 78, Appl
423	48	100.0	8	6	US-11-053-228-10	Sequence 10, Appl	496	48	100.0	10	4	US-10-395-741B-61	Sequence 61, App
424	48	100.0	8	6	US-11-032-090-3	Sequence 3, Appl1	497	48	100.0	10	4	US-10-398-248-71	Sequence 71, Appl
425	48	100.0	8	6	US-11-015-730-3	Sequence 3, Appl1	498	48	100.0	10	4	US-10-398-248-71	Sequence 71, Appl
426	48	100.0	8	6	US-11-015-126-20	Sequence 20, Appl	499	48	100.0	10	4	US-10-463-113-73	Sequence 73, Appl
427	48	100.0	8	6	US-11-115-906-36	Sequence 36, Appl	500	48	100.0	10	4	US-10-126-962-27	Sequence 27, Appl
428	48	100.0	9	3	US-09-884-663A-25	Sequence 25, Appl	501	48	100.0	10	4	US-10-665-227-7	Sequence 7, Appl1
429	48	100.0	9	3	US-09-809-517A-5	Sequence 5, Appl1	502	48	100.0	10	4	US-10-720-460-8	Sequence 8, Appl1
430	48	100.0	9	3	US-09-854-280-18	Sequence 18, Appl	503	48	100.0	10	4	US-10-723-933-55	Sequence 55, Appl
431	48	100.0	9	3	US-09-821-883-15	Sequence 15, Appl	504	48	100.0	10	4	US-10-723-933-68	Sequence 68, Appl
432	48	100.0	9	3	US-09-854-208-18	Sequence 18, Appl	505	48	100.0	10	4	US-10-763-619-4	Sequence 4, Appl1
433	48	100.0	9	4	US-10-171-417-8	Sequence 8, Appl1	506	48	100.0	10	5	US-10-681-381B-47	Sequence 47, Appl
434	48	100.0	9	4	US-10-246-837-8	Sequence 8, Appl1	507	48	100.0	10	5	US-10-482-793-9	Sequence 9, Appl1
435	48	100.0	9	4	US-10-120-145-17	Sequence 17, Appl	508	48	100.0	10	5	US-10-416-456A-29	Sequence 29, Appl
436	48	100.0	9	4	US-10-203-013-27	Sequence 27, Appl	509	48	100.0	10	5	US-10-683-451-13	Sequence 13, Appl
437	48	100.0	9	4	US-10-303-043-29	Sequence 29, Appl	510	48	100.0	10	5	US-10-946-786-7	Sequence 7, Appl1
438	48	100.0	9	4	US-10-387-841-8	Sequence 8, Appl1	511	48	100.0	10	5	US-10-854-735-30	Sequence 30, Appl
439	48	100.0	9	4	US-10-136-187-27	Sequence 27, Appl	512	48	100.0	10	5	US-10-658-752-2	Sequence 2, Appl1
440	48	100.0	9	4	US-10-354-774-32	Sequence 32, Appl	513	48	100.0	10	5	US-10-835-533-30	Sequence 30, Appl
441	48	100.0	9	4	US-10-271-012-32	Sequence 32, Appl	514	48	100.0	10	5	US-10-968-432-60	Sequence 60, Appl
442	48	100.0	9	4	US-10-364-649-56	Sequence 56, Appl	515	48	100.0	10	5	US-10-949-685-1	Sequence 1, Appl1
443	48	100.0	9	4	US-10-665-227-6	Sequence 6, Appl1	516	48	100.0	10	5	US-10-917-844-108	Sequence 108, App
444	48	100.0	9	4	US-10-350-682-7	Sequence 7, Appl1	517	48	100.0	10	5	US-10-846-341-17	Sequence 17, Appl
445	48	100.0	9	4	US-10-729-122-32	Sequence 32, Appl	518	48	100.0	10	5	US-10-990-207-9	Sequence 9, Appl1
446	48	100.0	9	4	US-10-729-039-32	Sequence 32, Appl	519	48	100.0	10	5	US-10-501-071-12	Sequence 12, Appl
447	48	100.0	9	4	US-10-723-933-66	Sequence 66, Appl	520	48	100.0	10	5	US-10-496-905-640	Sequence 640, App
448	48	100.0	9	5	US-10-729-527-32	Sequence 32, Appl	521	48	100.0	10	5	US-10-496-905-641	Sequence 641, App
449	48	100.0	9	5	US-10-727-898-32	Sequence 32, Appl	522	48	100.0	10	5	US-10-496-905-642	Sequence 642, App
450	48	100.0	9	5	US-10-728-696-32	Sequence 32, Appl	523	48	100.0	10	5	US-10-496-905-643	Sequence 643, App
451	48	100.0	9	5	US-10-850-873-27	Sequence 27, Appl	524	48	100.0	10	5	US-10-496-905-644	Sequence 644, App
452	48	100.0	9	5	US-10-946-786-6	Sequence 6, Appl1	525	48	100.0	10	5	US-10-496-905-645	Sequence 645, App
453	48	100.0	9	5	US-10-899-771-28	Sequence 28, Appl	526	48	100.0	10	6	US-11-099-302-3	Sequence 3, Appl1
454	48	100.0	9	5	US-10-687-060-27	Sequence 27, Appl	527	48	100.0	11	3	US-09-773-866-2	Sequence 2, Appl1
455	48	100.0	9	5	US-10-485-048-27	Sequence 27, Appl	528	48	100.0	11	3	US-09-814-569-2	Sequence 2, Appl1
456	48	100.0	9	5	US-10-485-048-29	Sequence 29, Appl	529	48	100.0	11	3	US-09-887-853-11	Sequence 11, Appl
457	48	100.0	9	5	US-10-658-752-5	Sequence 5, Appl1	530	48	100.0	11	3	US-09-815-534A-8	Sequence 8, Appl1
458	48	100.0	9	5	US-10-944-496-16	Sequence 16, Appl	531	48	100.0	11	4	US-10-105-717-4	Sequence 4, Appl1
459	48	100.0	9	5	US-10-501-071-11	Sequence 11, Appl1	532	48	100.0	11	4	US-10-871-145-4	Sequence 4, Appl1
460	48	100.0	9	5	US-10-501-071-11	Sequence 11, Appl	533	48	100.0	11	4	US-10-380-932-1	Sequence 1, Appl1
461	48	100.0	9	5	US-10-413-537-25	Sequence 25, Appl	534	48	100.0	11	4	US-10-665-227-8	Sequence 8, Appl1
462	48	100.0	9	6	US-11-015-730-4	Sequence 15, Appl	535	48	100.0	11	4	US-10-685-105-26	Sequence 26, Appl
463	48	100.0	9	6	US-11-144-912-15	Sequence 15, Appl	536	48	100.0	11	4	US-10-467-048A-9	Sequence 9, Appl1
464	48	100.0	9	6	US-11-001-241-32	Sequence 32, Appl	537	48	100.0	11	4	US-10-723-933-59	Sequence 59, Appl
465	48	100.0	10	2	US-08-981-490B-5	Sequence 5, Appl1	538	48	100.0	11	4	US-10-723-933-64	Sequence 64, Appl

539	48	100.0	11	4	US-10-723-933-71	Sequence 71, Appl	612	48	100.0	14	2	US-08-464-363-76	Sequence 76, Appl
540	48	100.0	11	4	US-10-723-933-72	Sequence 72, Appl	613	48	100.0	14	3	US-09-374-671-58	Sequence 58, Appl
541	48	100.0	11	4	US-10-748-055-25	Sequence 25, Appl	614	48	100.0	14	3	US-09-823-266-1	Sequence 1, Appl
542	48	100.0	11	5	US-10-859-700-8	Sequence 8, Appl	615	48	100.0	14	3	US-09-900-330A-19	Sequence 19, Appl
543	48	100.0	11	5	US-10-946-786-8	Sequence 8, Appl	616	48	100.0	14	3	US-09-784-199-9	Sequence 9, Appl
544	48	100.0	11	5	US-10-683-547-11	Sequence 11, Appl	617	48	100.0	14	4	US-10-004-381-32	Sequence 32, Appl
545	48	100.0	11	5	US-10-612-358-8	Sequence 8, Appl	618	48	100.0	14	4	US-10-196-107A-58	Sequence 58, Appl
546	48	100.0	11	5	US-10-491-677-1	Sequence 1, Appl	619	48	100.0	14	4	US-10-155-419-1	Sequence 1, Appl
547	48	100.0	11	5	US-10-508-791-1	Sequence 1, Appl	620	48	100.0	14	4	US-10-357-822-30	Sequence 30, Appl
548	48	100.0	11	5	US-10-681-207-3	Sequence 3, Appl	621	48	100.0	14	4	US-10-463-113-76	Sequence 76, Appl
549	48	100.0	11	5	US-10-681-207-7	Sequence 7, Appl	622	48	100.0	14	4	US-10-456-129-16	Sequence 16, Appl
550	48	100.0	11	5	US-10-508-894-1	Sequence 1, Appl	623	48	100.0	14	4	US-10-247-539-100	Sequence 100, Appl
551	48	100.0	11	5	US-10-470-958-5	Sequence 5, Appl	624	48	100.0	14	4	US-10-257-884A-11	Sequence 11, Appl
552	48	100.0	11	5	US-10-508-822-1	Sequence 1, Appl	625	48	100.0	14	4	US-10-478-671-53	Sequence 15, Appl
553	48	100.0	11	5	US-10-511-055-10	Sequence 10, Appl	626	48	100.0	14	4	US-10-608-440-49	Sequence 49, Appl
554	48	100.0	11	6	US-11-014-187-49	Sequence 49, Appl	627	48	100.0	14	5	US-10-653-350-2	Sequence 2, Appl
555	48	100.0	12	3	US-09-921-992-83	Sequence 83, Appl	628	48	100.0	14	5	US-10-851-818B-7	Sequence 7, Appl
556	48	100.0	12	3	US-09-946-893-3	Sequence 3, Appl	629	48	100.0	14	5	US-10-975-582-32	Sequence 32, Appl
557	48	100.0	12	3	US-09-927-436-1	Sequence 1, Appl	630	48	100.0	15	3	US-09-374-671-53	Sequence 53, Appl
558	48	100.0	12	4	US-10-171-417-4	Sequence 4, Appl	631	48	100.0	15	3	US-09-821-883-16	Sequence 16, Appl
559	48	100.0	12	4	US-10-008-960-4	Sequence 4, Appl	632	48	100.0	15	3	US-09-921-992-85	Sequence 85, Appl
560	48	100.0	12	4	US-10-465-789A-47	Sequence 47, Appl	633	48	100.0	15	3	US-09-728-653-2	Sequence 2, Appl
561	48	100.0	12	4	US-10-081-736-10	Sequence 10, Appl	634	48	100.0	15	4	US-10-010-184A-4	Sequence 4, Appl
562	48	100.0	12	4	US-10-381-870-13	Sequence 13, Appl	635	48	100.0	15	4	US-10-196-107A-53	Sequence 53, Appl
563	48	100.0	12	4	US-10-665-227-9	Sequence 9, Appl	636	48	100.0	15	4	US-10-015-328-2	Sequence 2, Appl
564	48	100.0	12	4	US-10-723-933-61	Sequence 61, Appl	637	48	100.0	15	4	US-10-221-655-5	Sequence 5, Appl
565	48	100.0	12	5	US-10-659-549-63	Sequence 43, Appl	638	48	100.0	15	4	US-10-313-638-2	Sequence 2, Appl
566	48	100.0	12	5	US-10-946-786-9	Sequence 9, Appl	639	48	100.0	15	5	US-10-683-651-38	Sequence 38, Appl
567	48	100.0	12	5	US-10-842-989-9	Sequence 9, Appl	640	48	100.0	15	5	US-10-457-091-254	Sequence 254, Appl
568	48	100.0	12	5	US-10-854-735-31	Sequence 31, Appl	641	48	100.0	15	5	US-10-959-653-37	Sequence 37, Appl
569	48	100.0	12	5	US-10-486-678-10	Sequence 10, Appl	642	48	100.0	15	5	US-10-871-369-8	Sequence 8, Appl
570	48	100.0	12	5	US-10-473-571-9	Sequence 9, Appl	643	48	100.0	15	5	US-10-872-770-8	Sequence 8, Appl
571	48	100.0	12	5	US-10-835-533-31	Sequence 31, Appl	644	48	100.0	15	5	US-10-903-476-8	Sequence 8, Appl
572	48	100.0	12	5	US-10-868-247-10	Sequence 10, Appl	645	48	100.0	15	5	US-10-958-216-2	Sequence 2, Appl
573	48	100.0	12	5	US-10-473-524-9	Sequence 9, Appl	646	48	100.0	15	5	US-10-953-901-2	Sequence 2, Appl
574	48	100.0	12	5	US-10-954-924-8	Sequence 8, Appl	647	48	100.0	15	5	US-10-922-802-8	Sequence 8, Appl
575	48	100.0	12	5	US-10-974-559-83	Sequence 83, Appl	648	48	100.0	15	5	US-10-806-062-2	Sequence 2, Appl
576	48	100.0	12	6	US-11-102-757-3	Sequence 3, Appl	649	48	100.0	15	5	US-10-961-826-8	Sequence 8, Appl
577	48	100.0	12	6	US-11-033-489-47	Sequence 47, Appl	650	48	100.0	15	5	US-10-965-006-8	Sequence 8, Appl
578	48	100.0	12	6	US-11-043-611-13	Sequence 13, Appl	651	48	100.0	15	5	US-10-974-559-85	Sequence 85, Appl
579	48	100.0	13	3	US-09-821-883-17	Sequence 17, Appl	652	48	100.0	15	6	US-11-144-312-16	Sequence 16, Appl
580	48	100.0	13	3	US-09-823-266-2	Sequence 2, Appl	653	48	100.0	15	6	US-11-047-365-8	Sequence 8, Appl
581	48	100.0	13	3	US-09-823-266-3	Sequence 3, Appl	654	48	100.0	16	3	US-09-822-765A-1	Sequence 1, Appl
582	48	100.0	13	3	US-09-823-266-4	Sequence 4, Appl	655	48	100.0	16	3	US-09-809-517A-4	Sequence 4, Appl
583	48	100.0	13	3	US-09-823-266-5	Sequence 5, Appl	656	48	100.0	16	3	US-09-809-517A-29	Sequence 29, Appl
584	48	100.0	13	4	US-10-188-602-1	Sequence 1, Appl	657	48	100.0	16	3	US-09-367-309A-3	Sequence 3, Appl
585	48	100.0	13	4	US-10-108-195-13	Sequence 13, Appl	658	48	100.0	16	3	US-09-948-018-25	Sequence 25, Appl
586	48	100.0	13	4	US-10-140-045-32	Sequence 32, Appl	659	48	100.0	16	3	US-09-911-569-103	Sequence 103, Appl
587	48	100.0	13	4	US-10-222-952A-11	Sequence 11, Appl	660	48	100.0	16	3	US-09-911-569-105	Sequence 105, Appl
588	48	100.0	13	4	US-10-155-419-2	Sequence 2, Appl	661	48	100.0	16	3	US-09-405-632-168	Sequence 168, Appl
589	48	100.0	13	4	US-10-155-419-3	Sequence 3, Appl	662	48	100.0	16	4	US-10-104-610-19	Sequence 19, Appl
590	48	100.0	13	4	US-10-155-419-4	Sequence 4, Appl	663	48	100.0	16	4	US-10-200-879-103	Sequence 103, Appl
591	48	100.0	13	4	US-10-155-419-5	Sequence 5, Appl	664	48	100.0	16	4	US-10-200-879-105	Sequence 105, Appl
592	48	100.0	13	4	US-10-009-792A-1	Sequence 1, Appl	665	48	100.0	16	4	US-10-282-122A-43329	Sequence 43329, A
593	48	100.0	13	4	US-10-356-088-4	Sequence 64, Appl	666	48	100.0	16	5	US-10-681-881B-48	Sequence 48, Appl
594	48	100.0	13	4	US-10-414-760-24	Sequence 20, Appl	667	48	100.0	16	5	US-10-738-423-23	Sequence 23, Appl
595	48	100.0	13	4	US-10-385-415-87	Sequence 87, Appl	668	48	100.0	16	5	US-10-658-752-4	Sequence 4, Appl
596	48	100.0	13	4	US-10-676-299-11	Sequence 11, Appl	669	48	100.0	16	5	US-10-658-752-29	Sequence 29, Appl
597	48	100.0	13	4	US-10-676-296-11	Sequence 11, Appl	670	48	100.0	16	5	US-10-762-159-168	Sequence 168, Appl
598	48	100.0	13	4	US-10-706-116-21	Sequence 21, Appl	671	48	100.0	17	6	US-11-058-073-168	Sequence 168, Appl
599	48	100.0	13	4	US-10-799-326-54	Sequence 64, Appl	672	48	100.0	17	3	US-09-809-517A-32	Sequence 32, Appl
600	48	100.0	13	5	US-10-715-810-3	Sequence 3, Appl	673	48	100.0	17	3	US-09-051-013-6	Sequence 6, Appl
601	48	100.0	13	5	US-10-921-676-3	Sequence 3, Appl	674	48	100.0	17	3	US-09-230-846A-5	Sequence 5, Appl
602	48	100.0	13	5	US-10-456-905-634	Sequence 634, Appl	675	48	100.0	17	3	US-09-925-287-1	Sequence 1, Appl
603	48	100.0	13	5	US-10-456-905-635	Sequence 635, Appl	676	48	100.0	17	4	US-10-083-590-12	Sequence 12, Appl
604	48	100.0	13	5	US-10-456-905-636	Sequence 636, Appl	677	48	100.0	17	4	US-10-047-991-8	Sequence 8, Appl
605	48	100.0	13	5	US-10-496-905-637	Sequence 637, Appl	678	48	100.0	17	4	US-10-404-667-6	Sequence 6, Appl
606	48	100.0	13	5	US-10-496-905-638	Sequence 638, Appl	679	48	100.0	17	4	US-10-441-965-28	Sequence 28, Appl
607	48	100.0	13	5	US-10-496-905-639	Sequence 639, Appl	680	48	100.0	17	4	US-10-441-965-34	Sequence 34, Appl
608	48	100.0	13	5	US-10-496-905-648	Sequence 648, Appl	681	48	100.0	17	4	US-10-429-921-16	Sequence 16, Appl
609	48	100.0	13	6	US-11-016-126-10	Sequence 10, Appl	682	48	100.0	17	5	US-10-658-752-32	Sequence 32, Appl
610	48	100.0	13	6	US-11-132-241-40	Sequence 40, Appl	683	48	100.0	17	5	US-10-787-219A-40	Sequence 40, Appl
611	48	100.0	13	6	US-11-144-912-17	Sequence 17, Appl	684	48	100.0	17	5	US-10-429-921-16	Sequence 16, Appl

685	48	100.0	18	2	US-08-954-771-47	Sequence 47, Appl	758	48	100.0	21	3	US-09-841-894-41	Sequence 41, Appl
686	48	100.0	18	2	US-08-462-386D-47	Sequence 47, Appl	759	48	100.0	21	3	US-09-991-681-33	Sequence 29, Appl
687	48	100.0	18	3	US-09-809-517A-1	Sequence 1, Appl	760	48	100.0	21	3	US-09-193-881-23	Sequence 23, Appl
688	48	100.0	18	3	US-09-864-761-34373	Sequence 34373, A	761	48	100.0	21	3	US-09-736-084-98	Sequence 98, Appl
689	48	100.0	18	3	US-09-849-243-17	Sequence 17, Appl	762	48	100.0	21	3	US-09-049-695A-22	Sequence 22, Appl
690	48	100.0	18	3	US-09-876-804A-92	Sequence 92, Appl	763	48	100.0	21	3	US-09-092-297-22	Sequence 22, Appl
691	48	100.0	18	3	US-09-795-872-1	Sequence 1, Appl	764	48	100.0	21	3	US-09-092-296-20	Sequence 20, Appl
692	48	100.0	18	3	US-09-736-476-47	Sequence 47, Appl	765	48	100.0	21	3	US-09-104-408-37	Sequence 37, Appl
693	48	100.0	18	4	US-10-105-717-3	Sequence 3, Appl	766	48	100.0	21	3	US-09-939-126-8	Sequence 8, Appl
694	48	100.0	18	4	US-10-371-145-3	Sequence 3, Appl	767	48	100.0	21	3	US-09-939-126-9	Sequence 9, Appl
695	48	100.0	18	4	US-10-383-675-45	Sequence 45, Appl	768	48	100.0	21	3	US-09-939-126-10	Sequence 10, Appl
696	48	100.0	18	4	US-10-100-699-3	Sequence 3, Appl	769	48	100.0	21	3	US-09-939-126-11	Sequence 11, Appl
697	48	100.0	18	4	US-10-662-824-1	Sequence 1, Appl	770	48	100.0	21	3	US-09-939-126-12	Sequence 12, Appl
698	48	100.0	18	4	US-10-815-402-22	Sequence 22, Appl	771	48	100.0	21	3	US-09-832-464-21	Sequence 21, Appl
699	48	100.0	18	5	US-10-647-654-47	Sequence 47, Appl	772	48	100.0	21	3	US-09-104-750-53	Sequence 53, Appl
700	48	100.0	18	5	US-10-835-517-47	Sequence 47, Appl	773	48	100.0	21	3	US-09-089-140-31	Sequence 31, Appl
701	48	100.0	18	5	US-10-914-165-45	Sequence 45, Appl	774	48	100.0	21	4	US-09-789-210-76	Sequence 76, Appl
702	48	100.0	18	5	US-10-658-752-1	Sequence 1, Appl	775	48	100.0	21	4	US-10-000-628-11	Sequence 11, Appl
703	48	100.0	18	5	US-10-957-433-92	Sequence 92, Appl	776	48	100.0	21	4	US-10-025-167-51	Sequence 51, Appl
704	48	100.0	18	5	US-10-716-095A-7	Sequence 7, Appl	777	48	100.0	21	4	US-10-082-659-16	Sequence 16, Appl
705	48	100.0	18	5	US-10-500-307-3	Sequence 3, Appl	778	48	100.0	21	4	US-10-216-408-27	Sequence 27, Appl
706	48	100.0	19	3	US-09-849-243-12	Sequence 12, Appl	779	48	100.0	21	4	US-10-060-275-5	Sequence 5, Appl
707	48	100.0	19	3	US-09-933-999A-31	Sequence 31, Appl	780	48	100.0	21	4	US-10-278-547-49	Sequence 49, Appl
708	48	100.0	19	3	US-09-996-069-13	Sequence 13, Appl	781	48	100.0	21	4	US-10-010-160-68	Sequence 68, Appl
709	48	100.0	19	3	US-09-876-904A-627	Sequence 627, Appl	782	48	100.0	21	4	US-10-338-395-29	Sequence 29, Appl
710	48	100.0	19	4	US-10-342-103-17	Sequence 17, Appl	783	48	100.0	21	4	US-10-185-567-25	Sequence 25, Appl
711	48	100.0	19	4	US-10-219-700-32	Sequence 32, Appl	784	48	100.0	21	4	US-10-191-252-13	Sequence 13, Appl
712	48	100.0	19	4	US-10-293-580-72	Sequence 72, Appl	785	48	100.0	21	4	US-10-192-254-33	Sequence 33, Appl
713	48	100.0	19	4	US-10-279-733-18	Sequence 18, Appl	786	48	100.0	21	4	US-10-449-462-104	Sequence 104, App
714	48	100.0	19	5	US-10-968-517-31	Sequence 31, Appl	787	48	100.0	21	4	US-10-417-997-16	Sequence 16, Appl
715	48	100.0	20	3	US-09-096-749A-114	Sequence 114, App	788	48	100.0	21	4	US-10-441-965-27	Sequence 27, Appl
716	48	100.0	20	3	US-09-051-013-3	Sequence 3, Appl	789	48	100.0	21	4	US-10-441-965-33	Sequence 33, Appl
717	48	100.0	20	3	US-09-320-907B-5	Sequence 5, Appl	790	48	100.0	21	4	US-10-646-873-49	Sequence 49, Appl
718	48	100.0	20	3	US-09-903-412-114	Sequence 114, App	791	48	100.0	21	4	US-10-448-525-37	Sequence 37, Appl
719	48	100.0	20	3	US-09-300-425B-26	Sequence 26, Appl	792	48	100.0	21	4	US-10-763-992-35	Sequence 35, Appl
720	48	100.0	20	4	US-10-174-117A-114	Sequence 114, App	793	48	100.0	21	4	US-10-296-085A-35	Sequence 36, Appl
721	48	100.0	20	4	US-10-165-155-114	Sequence 114, App	794	48	100.0	21	4	US-10-377-268-8	Sequence 8, Appl
722	48	100.0	20	4	US-10-190-162-114	Sequence 114, App	795	48	100.0	21	4	US-10-730-488-98	Sequence 98, Appl
723	48	100.0	20	4	US-10-408-930-32	Sequence 32, Appl	796	48	100.0	21	5	US-10-626-370-8	Sequence 8, Appl
724	48	100.0	20	4	US-10-192-832-52	Sequence 52, Appl	797	48	100.0	21	5	US-10-626-370-9	Sequence 9, Appl
725	48	100.0	20	4	US-10-192-832-53	Sequence 53, Appl	798	48	100.0	21	5	US-10-626-370-10	Sequence 10, Appl
726	48	100.0	20	4	US-10-321-558-6	Sequence 6, Appl	799	48	100.0	21	5	US-10-626-370-11	Sequence 11, Appl
727	48	100.0	20	4	US-10-447-292-5	Sequence 5, Appl	800	48	100.0	21	5	US-10-626-370-12	Sequence 12, Appl
728	48	100.0	20	4	US-10-420-564-6	Sequence 6, Appl	801	48	100.0	21	5	US-10-926-217-22	Sequence 22, Appl
729	48	100.0	20	4	US-10-456-129-14	Sequence 14, Appl	802	48	100.0	21	5	US-10-925-448-20	Sequence 20, Appl
730	48	100.0	20	4	US-10-250-859-7	Sequence 7, Appl	803	48	100.0	21	5	US-10-924-029-5	Sequence 5, Appl
731	48	100.0	20	5	US-10-742-887-48	Sequence 48, Appl	804	48	100.0	21	5	US-10-769-098-16	Sequence 16, Appl
732	48	100.0	20	5	US-10-820-467-274	Sequence 274, App	805	48	100.0	21	5	US-10-499-298-6	Sequence 6, Appl
733	48	100.0	20	5	US-10-808-248A-7	Sequence 7, Appl	806	48	100.0	21	5	US-10-771-833-6	Sequence 6, Appl
734	48	100.0	20	5	US-10-870-399-6	Sequence 6, Appl	807	48	100.0	21	5	US-10-738-780-23	Sequence 23, Appl
735	48	100.0	20	5	US-10-984-958A-19	Sequence 19, Appl	808	48	100.0	21	5	US-10-901-897-21	Sequence 21, Appl
736	48	100.0	20	5	US-10-871-369-7	Sequence 7, Appl	809	48	100.0	21	5	US-10-489-739-37	Sequence 37, Appl
737	48	100.0	20	5	US-10-872-770-7	Sequence 7, Appl	810	48	100.0	21	5	US-10-886-949-6	Sequence 6, Appl
738	48	100.0	20	5	US-10-903-476-7	Sequence 7, Appl	811	48	100.0	21	5	US-10-988-091-33	Sequence 33, Appl
739	48	100.0	20	5	US-10-958-216-1	Sequence 1, Appl	812	48	100.0	21	5	US-10-449-648-114	Sequence 104, App
740	48	100.0	20	5	US-10-953-901-1	Sequence 1, Appl	813	48	100.0	21	5	US-10-750-887-14	Sequence 14, Appl
741	48	100.0	20	5	US-10-922-802-7	Sequence 7, Appl	814	48	100.0	21	5	US-10-789-818-8	Sequence 8, Appl
742	48	100.0	20	5	US-10-806-062-1	Sequence 1, Appl	815	48	100.0	21	5	US-10-719-144-23	Sequence 23, Appl
743	48	100.0	20	5	US-10-961-826-7	Sequence 7, Appl	816	48	100.0	21	6	US-11-007-835-3	Sequence 30, Appl
744	48	100.0	20	5	US-10-965-006-7	Sequence 7, Appl	817	48	100.0	21	6	US-11-007-835-22	Sequence 22, Appl
745	48	100.0	20	6	US-11-047-365-7	Sequence 7, Appl	818	48	100.0	21	6	US-11-049-923-33	Sequence 33, Appl
746	48	100.0	21	2	US-08-926-626-13	Sequence 13, Appl	819	48	100.0	21	6	US-11-043-675-31	Sequence 31, Appl
747	48	100.0	21	3	US-09-050-516-49	Sequence 49, Appl	820	48	100.0	21	6	US-11-115-678-22	Sequence 22, Appl
748	48	100.0	21	3	US-09-276-600-11	Sequence 11, Appl	821	48	100.0	21	6	US-11-122-741-37	Sequence 37, Appl
749	48	100.0	21	3	US-09-065-383-33	Sequence 33, Appl	822	48	100.0	21	6	US-11-126-456-22	Sequence 22, Appl
750	48	100.0	21	3	US-09-099-823-27	Sequence 27, Appl	823	48	100.0	21	6	US-11-021-823-68	Sequence 68, Appl
751	48	100.0	21	3	US-09-234-717-25	Sequence 25, Appl	824	48	100.0	21	6	US-11-155-612-11	Sequence 11, Appl
752	48	100.0	21	3	US-09-850-178-19	Sequence 19, Appl	825	48	100.0	22	3	US-09-331-631A-16	Sequence 16, Appl
753	48	100.0	21	3	US-09-193-538-23	Sequence 23, Appl	826	48	100.0	22	4	US-09-911-569-102	Sequence 102, App
754	48	100.0	21	3	US-09-250-883-23	Sequence 23, Appl	827	48	100.0	22	4	US-10-200-879-102	Sequence 102, App
755	48	100.0	21	3	US-09-096-259-33	Sequence 33, Appl	828	48	100.0	22	4	US-10-147-095-16	Sequence 16, Appl
756	48	100.0	21	3	US-09-215-652-48	Sequence 48, Appl	829	48	100.0	23	3	US-09-939-126-7	Sequence 7, Appl
757	48	100.0	21	3	US-09-347-064-18	Sequence 18, Appl	830	48	100.0	23	3	US-09-897-776A-31	Sequence 31, Appl

831	48	100.0	23	3	US-09-969-748C-26	Sequence 26, Appl	904	48	100.0	26	5	US-10-766-102-25	Sequence 25, Appl
832	48	100.0	23	3	US-09-949-039-6	Sequence 6, Appl	905	48	100.0	26	5	US-10-877-952-25	Sequence 25, Appl
833	48	100.0	23	4	US-10-105-717-5	Sequence 5, Appl	906	48	100.0	27	3	US-09-846-729A-22	Sequence 22, Appl
834	48	100.0	23	4	US-10-171-417-5	Sequence 5, Appl	907	48	100.0	27	3	US-09-846-729A-26	Sequence 26, Appl
835	48	100.0	23	4	US-10-171-417-6	Sequence 6, Appl	908	48	100.0	27	3	US-09-898-461-9	Sequence 9, Appl
836	48	100.0	23	4	US-10-771-145-5	Sequence 5, Appl	909	48	100.0	27	4	US-10-342-103-4	Sequence 4, Appl
837	48	100.0	23	4	US-10-354-774-24	Sequence 24, Appl	910	48	100.0	27	4	US-10-441-667-22	Sequence 22, Appl
838	48	100.0	23	4	US-10-271-012-24	Sequence 24, Appl	911	48	100.0	27	4	US-10-441-667-26	Sequence 26, Appl
839	48	100.0	23	4	US-10-465-789A-48	Sequence 48, Appl	912	48	100.0	27	4	US-10-029-386-30005	Sequence 30005, A
840	48	100.0	23	4	US-10-729-122-24	Sequence 24, Appl	913	48	100.0	27	4	US-10-275-589-21	Sequence 21, Appl
841	48	100.0	23	4	US-10-729-039-24	Sequence 24, Appl	914	48	100.0	27	5	US-10-675-982-9	Sequence 9, Appl
842	48	100.0	23	4	US-10-350-555-56	Sequence 56, Appl	915	48	100.0	28	3	US-09-897-776A-10	Sequence 10, Appl
843	48	100.0	23	4	US-10-344-607-2	Sequence 2, Appl	916	48	100.0	28	3	US-09-774-954-14	Sequence 14, Appl
844	48	100.0	23	4	US-10-625-047-56	Sequence 56, Appl	917	48	100.0	28	5	US-10-766-102-20	Sequence 20, Appl
845	48	100.0	23	5	US-10-622-088-92	Sequence 92, Appl	918	48	100.0	28	5	US-10-877-952-20	Sequence 20, Appl
846	48	100.0	23	5	US-10-622-088-97	Sequence 97, Appl	919	48	100.0	29	3	US-09-880-901-2	Sequence 2, Appl
847	48	100.0	23	5	US-10-470-987-15	Sequence 15, Appl	920	48	100.0	29	3	US-09-962-756-22202	Sequence 2202, Ap
848	48	100.0	23	5	US-10-729-527-24	Sequence 24, Appl	921	48	100.0	29	4	US-10-282-121-12	Sequence 12, Appl
849	48	100.0	23	5	US-10-727-898-24	Sequence 24, Appl	922	48	100.0	29	4	US-10-149-085-14	Sequence 14, Appl
850	48	100.0	23	5	US-10-728-696-24	Sequence 24, Appl	923	48	100.0	29	4	US-10-029-386-30014	Sequence 30014, A
851	48	100.0	23	5	US-10-626-370-7	Sequence 7, Appl	924	48	100.0	29	4	US-10-253-471-2202	Sequence 2202, Ap
852	48	100.0	23	5	US-10-631-258-56	Sequence 56, Appl	925	48	100.0	29	4	US-10-297-585-2	Sequence 2, Appl
853	48	100.0	23	5	US-10-495-715-70	Sequence 70, Appl	926	48	100.0	29	4	US-10-692-151-41	Sequence 41, Appl
854	48	100.0	23	5	US-10-766-102-31	Sequence 31, Appl	927	48	100.0	29	4	US-10-692-151-42	Sequence 42, Appl
855	48	100.0	23	5	US-10-966-097A-6	Sequence 6, Appl	928	48	100.0	29	4	US-10-692-151-43	Sequence 43, Appl
856	48	100.0	23	5	US-10-495-905-652	Sequence 652, App	929	48	100.0	29	4	US-10-692-151-44	Sequence 44, Appl
857	48	100.0	23	6	US-11-034-275-42	Sequence 42, Appl	930	48	100.0	29	4	US-10-692-151-45	Sequence 45, Appl
858	48	100.0	23	6	US-11-033-489-48	Sequence 48, Appl	931	48	100.0	29	4	US-10-692-151-46	Sequence 46, Appl
859	48	100.0	23	6	US-11-001-241-24	Sequence 24, Appl	932	48	100.0	29	4	US-10-692-151-47	Sequence 47, Appl
860	48	100.0	24	3	US-09-841-132-221	Sequence 221, App	933	48	100.0	29	4	US-10-692-151-48	Sequence 48, Appl
861	48	100.0	24	3	US-09-834-465-8	Sequence 8, Appl	934	48	100.0	29	5	US-10-489-386-39	Sequence 39, Appl
862	48	100.0	24	4	US-10-080-455-5	Sequence 9, Appl	935	48	100.0	29	5	US-10-877-952-117	Sequence 117, App
863	48	100.0	24	4	US-10-112-193-9	Sequence 9, Appl	936	48	100.0	29	5	US-10-757-720-2	Sequence 2, Appl
864	48	100.0	24	4	US-10-189-916A-2	Sequence 2, Appl	937	48	100.0	30	3	US-09-664-761-36251	Sequence 36251, A
865	48	100.0	24	4	US-10-713-391-5	Sequence 5, Appl	938	48	100.0	30	3	US-09-754-826-3	Sequence 3, Appl
866	48	100.0	24	5	US-10-872-155-221	Sequence 221, App	939	48	100.0	30	3	US-09-911-569-98	Sequence 98, Appl
867	48	100.0	24	5	US-10-861-685-8	Sequence 8, Appl	940	48	100.0	30	3	US-09-911-569-100	Sequence 100, App
868	48	100.0	24	5	US-10-652-879-8	Sequence 8, Appl	941	48	100.0	30	3	US-09-911-569-104	Sequence 104, App
869	48	100.0	24	5	US-10-750-887-10	Sequence 10, Appl	942	48	100.0	30	4	US-10-200-879-98	Sequence 98, Appl
870	48	100.0	24	5	US-10-496-905-647	Sequence 647, App	943	48	100.0	30	4	US-10-200-879-100	Sequence 100, App
871	48	100.0	24	6	US-11-033-489-121	Sequence 121, App	944	48	100.0	30	4	US-10-200-879-104	Sequence 104, App
872	48	100.0	24	6	US-11-032-294-22	Sequence 22, Appl	945	48	100.0	30	4	US-10-192-832-66	Sequence 66, Appl
873	48	100.0	25	3	US-09-864-761-45218	Sequence 45218, A	946	48	100.0	30	4	US-10-192-832-67	Sequence 67, Appl
874	48	100.0	25	3	US-09-911-569-96	Sequence 96, Appl	947	48	100.0	30	4	US-10-192-832-76	Sequence 76, Appl
875	48	100.0	25	3	US-09-897-776A-22	Sequence 22, Appl	948	48	100.0	30	4	US-10-385-832-76	Sequence 149, App
876	48	100.0	25	3	US-10-200-879-96	Sequence 96, Appl	949	48	100.0	30	4	US-10-227-012-5	Sequence 5, Appl
877	48	100.0	25	4	US-10-321-846-5	Sequence 5, Appl	950	48	100.0	30	5	US-10-650-280-11	Sequence 11, Appl
878	48	100.0	25	4	US-10-432-905-5	Sequence 5, Appl	951	48	100.0	31	3	US-09-925-442-37	Sequence 37, Appl
879	48	100.0	25	4	US-10-451-926-5	Sequence 5, Appl	952	48	100.0	31	3	US-09-925-442-37	Sequence 58, Appl
880	48	100.0	25	4	US-10-469-140-5	Sequence 5, Appl	953	48	100.0	31	3	US-09-966-069-4	Sequence 4, Appl
881	48	100.0	25	4	US-10-468-454-5	Sequence 5, Appl	954	48	100.0	31	3	US-09-966-069-12	Sequence 12, Appl
882	48	100.0	25	4	US-10-467-823-5	Sequence 5, Appl	955	48	100.0	31	3	US-09-962-756-2203	Sequence 2203, Ap
883	48	100.0	25	4	US-10-759-138-5	Sequence 5, Appl	956	48	100.0	31	4	US-10-003-681-1	Sequence 1, Appl
884	48	100.0	25	4	US-10-344-607-14	Sequence 14, Appl	957	48	100.0	31	4	US-10-253-471-2203	Sequence 2203, Ap
885	48	100.0	25	4	US-10-344-607-18	Sequence 18, Appl	958	48	100.0	31	4	US-10-253-471-2203	Sequence 2203, Ap
886	48	100.0	25	4	US-10-482-793-29	Sequence 29, Appl	959	48	100.0	31	5	US-10-766-102-35	Sequence 35, Appl
887	48	100.0	25	5	US-10-766-102-22	Sequence 22, Appl	960	48	100.0	31	6	US-11-040-686-82	Sequence 29, Appl
888	48	100.0	25	5	US-10-481-013A-5	Sequence 5, Appl	961	48	100.0	32	3	US-09-906-179A-214	Sequence 214, App
889	48	100.0	25	5	US-10-978-413-5	Sequence 5, Appl	962	48	100.0	32	4	US-10-450-295-4	Sequence 4, Appl
890	48	100.0	25	5	US-10-916-448-5	Sequence 5, Appl	963	48	100.0	32	5	US-10-997-651-27	Sequence 27, Appl
891	48	100.0	25	5	US-10-959-509-5	Sequence 5, Appl	964	48	100.0	32	5	US-09-839-577A-6	Sequence 6, Appl
892	48	100.0	25	5	US-10-959-509-5	Sequence 5, Appl	965	48	100.0	33	3	US-09-259-658-49	Sequence 49, Appl
893	48	100.0	25	5	US-10-978-331-5	Sequence 5, Appl	966	48	100.0	33	3	US-09-259-658-50	Sequence 50, Appl
894	48	100.0	25	5	US-10-507-611-5	Sequence 5, Appl	967	48	100.0	33	3	US-09-866-538-21	Sequence 21, Appl
895	48	100.0	25	5	US-10-773-385-18	Sequence 18, Appl	968	48	100.0	33	3	US-09-897-776A-28	Sequence 28, Appl
896	48	100.0	26	3	US-09-664-761-47310	Sequence 47310, A	969	48	100.0	33	3	US-10-121-308-21	Sequence 21, Appl
897	48	100.0	26	3	US-09-897-776A-25	Sequence 25, Appl	970	48	100.0	33	4	US-10-455-713-7	Sequence 22, Appl
898	48	100.0	26	4	US-10-209-041-12	Sequence 12, Appl	971	48	100.0	33	4	US-10-455-713-7	Sequence 6, Appl
899	48	100.0	26	4	US-10-385-415-147	Sequence 147, App	972	48	100.0	33	4	US-10-455-713-7	Sequence 2, Appl
900	48	100.0	26	4	US-10-433-452A-46	Sequence 46, Appl	973	48	100.0	33	4		
901	48	100.0	26	4			974	48	100.0	33	4		
902	48	100.0	26	4			975	48	100.0	33	4		
903	48	100.0	26	4			976	48	100.0	33	4		

```
977 48 100.0 33 4 US-10-723-947-144 Sequence 144, App
978 48 100.0 33 3 US-10-723-947-145 Sequence 145, App
979 48 100.0 33 5 US-10-759-762-2 Sequence 2, Appl
980 48 100.0 33 5 US-10-885-988-21 Sequence 21, Appl
981 48 100.0 33 5 US-10-766-102-28 Sequence 22, Appl
982 48 100.0 33 5 US-10-931-304-22 Sequence 28, Appl
983 48 100.0 34 4 US-10-417-923-21 Sequence 21, Appl
984 48 100.0 34 5 US-10-450-763-41501 Sequence 41501, A
985 48 100.0 34 5 US-10-997-651-26 Sequence 26, Appl
986 48 100.0 34 5 US-10-997-651-28 Sequence 26, Appl
987 48 100.0 35 3 US-09-862-756-2204 Sequence 2204, Ap
988 48 100.0 35 4 US-10-083-815-68 Sequence 68, Appl
989 48 100.0 35 4 US-10-253-471-2204 Sequence 2204, Ap
990 48 100.0 35 4 US-10-253-493-2204 Sequence 2204, Ap
991 48 100.0 35 4 US-10-425-115-194568 Sequence 194568,
992 48 100.0 35 5 US-10-997-651-24 Sequence 24, Appl
993 48 100.0 35 5 US-10-997-651-25 Sequence 25, Appl
994 48 100.0 35 5 US-10-997-651-29 Sequence 29, Appl
995 48 100.0 36 3 US-09-276-455-8 Sequence 8, Appl
996 48 100.0 36 4 US-10-216-289-12 Sequence 12, Appl
997 48 100.0 36 5 US-10-474-298-33 Sequence 33, Appl
998 48 100.0 37 3 US-09-575-847-5 Sequence 5, Appl
999 48 100.0 37 3 US-09-911-569-97 Sequence 97, Appl
1000 48 100.0 37 4 US-10-200-879-97 Sequence 97, Appl
```

ALIGNMENTS

RESULT 1

US-09-280-030-61

```
; Sequence 61, Application US/09280030A
; Patent No. US20010021515A1
```

GENERAL INFORMATION:

```
; APPLICANT: Sato, Seiji
; APPLICANT: Higashikuni, Naohiko
; APPLICANT: Kudo, Toshiyuki
; APPLICANT: Kondo, Masaaki
; TITLE OF INVENTION: DNAS ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
; TITLE OF INVENTION: PREPARING USEFUL POLYPEPTIDES THROUGH EXPRESSION OF THE
; TITLE OF INVENTION: DNAS
; FILE REFERENCE: 382.1026
; CURRENT APPLICATION NUMBER: US/09/280.030A
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: JP10-87339/1998
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 61
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designated is
; OTHER INFORMATION: a tag for separation/purification of a fusion
; OTHER INFORMATION: protein
US-09-280-030-61
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6
```

RESULT 2

US-09-771-956-11

```
; Sequence 11, Application US/097719956
; Patent No. US20010031474A1
```

GENERAL INFORMATION:

APPLICANT: Bennett, Michele

```
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771.956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HEXAHISTADINE
; OTHER INFORMATION: TAG
US-09-771-956-11

Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6
```

RESULT 3

US-09-822-485-30

```
; Sequence 30, Application US/09822485
; Patent No. US20020001825A1
```

GENERAL INFORMATION:

```
; APPLICANT: Itoh, No. US20020001825A1yuki
; TITLE OF INVENTION: NO. US20020001825A1el Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 08035.0001-01000
; CURRENT APPLICATION NUMBER: US/09/822.485
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: protein tag
US-09-822-485-30
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6
```

RESULT 4

US-09-760-008A-9

```
; Sequence 9, Application US/09760008A
; Patent No. US20020004483A1
```

GENERAL INFORMATION:

```
; APPLICANT: NISSEN, TORBEN LAUSGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/09/760.008A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176.376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189.506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215.644
```

```

; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-760-008A-9
```

```

Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```

RESULT 5
US-09-728-911-12
; Sequence 12, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenteng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-93
; CURRENT APPLICATION NUMBER: US/09/728,911
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/169,049
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/232,219
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/244,610
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His Tag amino acid sequence
US-09-728-911-12
```

```

Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```

RESULT 6
US-09-313-942-1
; Sequence 1, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: AND USING
```

```

; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tag sequence
US-09-313-942-1
```

```

Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```

RESULT 7
US-09-809-517A-11
; Sequence 11, Application US/09809517A
; Patent No. US20020034733A1
; GENERAL INFORMATION:
; APPLICANT: Lobnitz, Corinna
; TITLE OF INVENTION: No. US20020034733A1 methods for displaying (poly)peptides/pro
; FILE REFERENCE: MORPHO/11
; CURRENT APPLICATION NUMBER: US/09/809,517A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-11
```

```

Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```

RESULT 8
US-09-211-691-14
; Sequence 14, Application US/09211691
; Patent No. US20020034805A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Young, N. Martin
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Fusion Proteins for Use in Enzymatic Synthesis of
; FILE REFERENCE: 019957-012910US
; CURRENT APPLICATION NUMBER: US/09/211,691
```

```
/ CURRENT FILING DATE: 1998-12-14
/ PRIOR APPLICATION NUMBER: US 60/069,443
/ PRIOR FILING DATE: 1997-12-15
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:6-His tail for
US-09-211-691-14
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 9
US-09-808-037-33
/ Sequence 33, Application US/09808037
/ Patent No. US20020052311A1
/ GENERAL INFORMATION:
/ APPLICANT: SOLOMON, Beki
/ APPLICANT: HANAN, Eliat
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
/ TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
/ FILE REFERENCE: SOLOMON-2D
/ CURRENT APPLICATION NUMBER: US/09/808,037
/ CURRENT FILING DATE: 2001-03-15
/ PRIOR APPLICATION NUMBER: 09/629,971
/ PRIOR FILING DATE: 2000-07-31
/ PRIOR APPLICATION NUMBER: US 09/473,653
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: US 60/152,417
/ PRIOR FILING DATE: 1999-09-03
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 33
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: synthetic construct
US-09-808-037-33
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 10
US-09-888-615-149
/ Sequence 149, Application US/09888615
/ Patent No. US20020064856A1
/ GENERAL INFORMATION:
/ APPLICANT: PLOWMAN, GREGORY
/ APPLICANT: WAYTE, DAVID
/ APPLICANT: CAENEPEEL, SEAN
/ APPLICANT: CHARYDCZAK, GLEN
/ APPLICANT: MANNING, GERARD
/ APPLICANT: SUDARSANAM, SUCHA
/ TITLE OF INVENTION: NOVEL PROTEASES
/ FILE REFERENCE: 038602/1214
/ CURRENT APPLICATION NUMBER: US/09/888,615
/ CURRENT FILING DATE: 2001-06-26
```

```
/ PRIOR APPLICATION NUMBER: 60/214,047
/ PRIOR FILING DATE: 2000-06-26
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 149
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: His tag
US-09-888-615-149
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 11
US-09-875-519A-26
/ Sequence 26, Application US/09875519A
/ Patent No. US20020068059A1
/ GENERAL INFORMATION:
/ APPLICANT: Farries, Timothy C.
/ APPLICANT: Harrison, Richard A.
/ TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
/ FILE REFERENCE: 4-30443/A/IMU/PCT
/ CURRENT APPLICATION NUMBER: US/09/875,519A
/ PRIOR APPLICATION NUMBER: 2001-06-06
/ PRIOR FILING DATE: 1997-03-04
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 26
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: amino acid
/ OTHER INFORMATION: Insertion
US-09-875-519A-26
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 12
US-09-367-309A-4
/ Sequence 4, Application US/09367309A
/ Publication No. US20020081329A1
/ GENERAL INFORMATION:
/ APPLICANT: MACFARLAN, RODERICK I.
/ APPLICANT: MALIAROS, JIM
/ TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
/ FILE REFERENCE: 017227/0149
/ CURRENT APPLICATION NUMBER: US/09/367,309A
/ CURRENT FILING DATE: 1999-08-11
/ PRIOR APPLICATION NUMBER: PCT/AU98/00080
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: AU PO 5178
/ PRIOR FILING DATE: 1997-02-19
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 6
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-367-309A-4
Query Match
Best Local Similarity 100.0%; Score 48; DB 3; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
   1 HHHHH 6
Db 1 HHHHH 6

RESULT 13
US-09-837-992-44
; Sequence 44, Application US/09837992
; Patent No. US20020081687A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Schultz, Joshua
; APPLICANT: Shan, Bei
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Sticosterolemia Susceptibility Gene (SSG) : Compositions
; FILE REFERENCE: 018781-006020US
; CURRENT APPLICATION NUMBER: US/09/837,992
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,465
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/204,234
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:6-His epitope
; US-09-837-992-44
Query Match
Best Local Similarity 100.0%; Score 48; DB 3; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
   1 HHHHH 6
Db 1 HHHHH 6

RESULT 14
US-09-871-856-18
; Sequence 18, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US98 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO:18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-871-856-18
Query Match
Best Local Similarity 100.0%; Score 48; DB 3; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
   1 HHHHH 6
Db 1 HHHHH 6

RESULT 15
US-09-801-968-22
; Sequence 22, Application US/09801968
; Patent No. US20020082205A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020082205A1uyuki
; APPLICANT: Kavanagh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
; FILE REFERENCE: PP-17150.001/201130.40901
; CURRENT APPLICATION NUMBER: US/09/801,968
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His6 tag
; US-09-801-968-22
Query Match
Best Local Similarity 100.0%; Score 48; DB 3; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
   1 HHHHH 6
Db 1 HHHHH 6

RESULT 16
US-09-865-363-18
; Sequence 18, Application US/09865363
```

Publication No. US20020086826A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Marasovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,363
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-865-363-18
Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHH 6
DB 1 HHHHH 6
RESULT 17
US-09-871-291-18
Sequence 18, Application US/09871291
Publication No. US20020086827A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Marasovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,291
FILING DATE: 30-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-871-291-18
Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHH 6
DB 1 HHHHH 6
RESULT 18
US-09-875-338-93
Sequence 93, Application US/09875338
Patent No. US20020095024A1
GENERAL INFORMATION:
APPLICANT: MIKESELL, GLEN E.
APPLICANT: CHANG, HAN
APPLICANT: PINGER, JOSHUA N.
APPLICANT: YANG, GUOCHEN
APPLICANT: ZHOU, XIA-DI
APPLICANT: LU, PIN
APPLICANT: PEACH, ROBERT
TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
TITLE OF INVENTION: IMMUNOMODULATION
FILE REFERENCE: 3053-4071US2
CURRENT APPLICATION NUMBER: US/09/875,338
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/272,107
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/209,811
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 93
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Epitope tag
US-09-875-338-93
Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 19

US-09-988-899-5
; Sequence 5, Application US/09988899
; Patent No. US20020102613A1
; GENERAL INFORMATION:
; APPLICANT: HOGGENBOOM, HENDRICUS R.J.M.
; TITLE OF INVENTION: NOVEL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE
; FILE REFERENCE: DX/003 CON
; CURRENT APPLICATION NUMBER: US/09/988,899
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/US00/13682
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 99201558.6
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6X-His tag
US-09-988-899-5

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 20

US-09-798-584-16
; Sequence 16, Application US/09798584
; Patent No. US20020102676A1
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: KCNB: A NO. US20020102676A1 Potassium Channel Protein
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09/798,584
; CURRENT FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6-His epitope
US-09-798-584-16

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 21

US-09-817-764-9
; Sequence 9, Application US/09817764
; Patent No. US20020102678A1
; GENERAL INFORMATION:
; APPLICANT: HAROCHE, JULIEN
; APPLICANT: ALLIGNET, JEANINE
; APPLICANT: EL SOLH, NEYANE
; TITLE OF INVENTION: STAPHYLOCOCCAL GENE, VGAC, CONFERRING RESISTANCE TO
; TITLE OF INVENTION: STREPTOGRAMIN A AND RELATED COMPOUNDS
; FILE REFERENCE: 03495.0201
; CURRENT APPLICATION NUMBER: US/09/817,764
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/197,372
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic His
US-09-817-764-9

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 22

US-09-943-382-1
; Sequence 1, Application US/09943382
; Publication No. US20020103230A1
; GENERAL INFORMATION:
; APPLICANT: RENHOME, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAVER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; APPLICANT: PECCHI, SABINA
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/09/943,382
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6X-His tag
US-09-943-382-1

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 23

US-09-951-265-2

```
/ Sequence 2, Application US/09951265
/ Publication No. US20020107392A1
/ GENERAL INFORMATION:
/ APPLICANT: RENHOME, PAUL A.
/ APPLICANT: BECCHI, SABINA
/ APPLICANT: MACHAJEWSKI, TIMOTHY D.
/ APPLICANT: SCHAFER, CYNTHIA M.
/ APPLICANT: TAYLOR, CLARKE
/ APPLICANT: MCCREA, WILLIAM R. JR
/ APPLICANT: MCBRIDE, CHRISTOPHER
/ APPLICANT: JAZAN, ELISA
/ TITLE OF INVENTION: QUINOLINONE DERIVATIVES
/ FILE REFERENCE: 072121/0141
/ CURRENT APPLICATION NUMBER: US/09/951,265
/ PRIOR FILING DATE: 2002-12-13
/ PRIOR APPLICATION NUMBER: 60/232,159
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6X
US-09-951-265-2
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
         |||||
Db       1 HHHHHH 6
```

```
RESULT 24
US-09-801-676A-2
/ Sequence 2, Application US/09801676A
/ Patent No. US20020114734A1
/ GENERAL INFORMATION:
/ APPLICANT: Pantoliano, Michael W.
/ APPLICANT: Bone, Roger F.
/ APPLICANT: Rhind, Alexander W.
/ APPLICANT: Saleme, Francis R.
/ TITLE OF INVENTION: Computer Program for Thermal Shift Assay
/ TITLE OF INVENTION: Apparatus for Ligand Development and
/ FILE REFERENCE: 1503.011000E
/ CURRENT APPLICATION NUMBER: US/09/801,676A
/ CURRENT FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 09/459,996
/ PRIOR FILING DATE: 1999-12-14
/ PRIOR APPLICATION NUMBER: 60/017,860
/ PRIOR FILING DATE: 1996-05-09
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 3.1
/ SEQ ID NO 2
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Six histidine epitope tag of His6D(III)-FGFR1
US-09-801-676A-2
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
         |||||
Db       1 HHHHHH 6
```

```
RESULT 25
US-09-916-940-99
/ Sequence 99, Application US/09916940
/ Patent No. US20020127564A1
/ GENERAL INFORMATION:
/ APPLICANT: No. US20020127564A1an, Gary P
/ TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
/ FILE REFERENCE: A-64260-6/RMS/RMS
/ CURRENT APPLICATION NUMBER: US/09/916,940
/ CURRENT FILING DATE: 2001-07-27
/ PRIOR APPLICATION NUMBER: US 09/727,715
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 08/963,368
/ PRIOR FILING DATE: 1997-11-03
/ PRIOR APPLICATION NUMBER: US 08/589,109
/ PRIOR FILING DATE: 1996-01-23
/ PRIOR APPLICATION NUMBER: US 08/589,911
/ PRIOR FILING DATE: 1996-01-23
/ PRIOR APPLICATION NUMBER: US 08/789,333
/ PRIOR FILING DATE: 1997-01-23
/ PRIOR APPLICATION NUMBER: US 08/787,738
/ PRIOR FILING DATE: 1997-01-23
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 99
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: histidine tag
US-09-916-940-99
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
         |||||
Db       1 HHHHHH 6
```

```
RESULT 26
US-09-780-933-14
/ Sequence 14, Application US/09780933
/ Patent No. US20020127652A1
/ GENERAL INFORMATION:
/ APPLICANT: SCHAMBE, HANS T.
/ APPLICANT: ANDERSEN, KIM V.
/ APPLICANT: VAN DEN HAZEL, BART
/ APPLICANT: CHRISTIANSEN, JESPER
/ APPLICANT: JEPSEN, CLAUD B.
/ TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
/ FILE REFERENCE: 31-001000US
/ CURRENT APPLICATION NUMBER: US/09/780,933
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: PA 2000 00220
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: 60/184,035
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: PA 2000 01092
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: 60/225,558
/ PRIOR FILING DATE: 2000-08-16
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
```

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-780-933-14

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
Db 1 HHHHHH 6

RESULT 27
US-09-900-530A-15
Sequence 15, Application US/09900530A
Patent No. US20020128438A1

GENERAL INFORMATION:
APPLICANT: Seol, Dae-Mu
APPLICANT: Billiar, Timothy R.
TITLE OF INVENTION: DNA Cassette for the Production of
TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus Vector, Their
FILE REFERENCE: 5006-1-002
CURRENT APPLICATION NUMBER: US/09/900,530A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: KR 2000-38441
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: His-tag
US-09-900-530A-15

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
Db 1 HHHHHH 6

RESULT 28
US-09-973-145-4
Sequence 4, Application US/09973145
Patent No. US20020132248A1

GENERAL INFORMATION:
APPLICANT: Rothschild, Kenneth J.
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Proteins
FILE REFERENCE: AMBER-06819
CURRENT APPLICATION NUMBER: US/09/973,145
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/382,950
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
NAME/KEY: misc_feature

OTHER INFORMATION: Synthetic
US-09-973-145-4

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
Db 1 HHHHHH 6

RESULT 29
US-09-731-558-11
Sequence 11, Application US/09731558
Patent No. US20020146691A1

GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Rebar, Edward J.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REFERENCE: 019496-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6xHis tag
US-09-731-558-11

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
Db 1 HHHHHH 6

RESULT 30
US-09-822-698A-22
Sequence 22, Application US/09822698A
Patent No. US20020146750A1

GENERAL INFORMATION:
APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Hendrickx, Maria P.G.
TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
FILE REFERENCE: DYX-015.1 US
CURRENT APPLICATION NUMBER: US/09/822,698A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 09/538,913
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Microsoft Word
SEQ ID NO 22
LENGTH: 6
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: hexahistidine peptide
US-09-822-698A-22

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 31

US-09-144-886-5
; Sequence 5, Application US/091444886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: His6
US-09-144-886-5

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 32

US-09-935-868-1
; Sequence 1, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tag sequence
US-09-935-868-1

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 33

US-09-877-650-18
; Sequence 18, Application US/09877650
; Patent No. US20020169117A1

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/877,650

FILING DATE: 08-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-877-650-18

Query Match 100.0%; Score 48; DB 3; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 34

US-09-814-604-9
; Sequence 9, Application US/09814604
; Publication No. US20030003517A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Elliott S.
; APPLICANT: Chandrasekhar Roshantha A.
; TITLE OF INVENTION: Methods of Detecting Dissociated Nuclear
; TITLE OF INVENTION: Hormone Receptor Ligands
; FILE REFERENCE: P-AR 4528
; CURRENT APPLICATION NUMBER: US/09/814,604
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: synthetic peptide
US-09-814-604-9

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 35

US-09-939-769-94
Sequence 94, Application US/09939769
Publication No. US20030017149A1
GENERAL INFORMATION:
APPLICANT: HOFFER, JAMES P.
APPLICANT: RUSSELL, MARIJANE
TITLE OF INVENTION: SINGLE CHAIN ANTIBODY FUSION REAGENTS THAT REGULATE
TITLE OF INVENTION: TRANSCRIPTION IN VIVO
FILE REFERENCE: 039322/0226
CURRENT APPLICATION NUMBER: US/09/939,769
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 08/728,890
PRIOR FILING DATE: 1996-10-10
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 94
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6-His tag
US-09-939-769-94

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 36

US-09-935-430-698
Sequence 698, Application US/09935430
Publication No. US20030017466A1
GENERAL INFORMATION:
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: CHALITA-ELD, PIA
APPLICANT: JAKOBOWITZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: OTHER CANCERS
FILE REFERENCE: 51158-20050.00
CURRENT APPLICATION NUMBER: US/09/935,430
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/282,739
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 700
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 698
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6-His tag
US-09-935-430-698

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 37

US-09-821-726-19
Sequence 19, Application US/09821726
Publication No. US20030017548A1
GENERAL INFORMATION:
APPLICANT: MARTIN, TERENCE E.
APPLICANT: TOBACK, F. GARY
APPLICANT: POWELL, C. THOMAS
APPLICANT: AGARWAL, KAN
TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
FILE REFERENCE: 21459/90913
CURRENT APPLICATION NUMBER: US/09/821,726
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic His
US-09-821-726-19

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 38

US-09-945-248B-3
Sequence 3, Application US/09945248B
Publication No. US20030017971A1
GENERAL INFORMATION:
APPLICANT: REED, ROBIN
APPLICANT: LUO, MING-JUAN
APPLICANT: ZHOU, ZHAOLAN
TITLE OF INVENTION: METHOD FOR INCREASING LEVELS OF EXPORT OF MENA FROM THE
TITLE OF INVENTION: NUCLEUS TO THE CYTOPLASM BY PROVIDING IN THE NUCLEUS
TITLE OF INVENTION: RECOMBINANT MAMMALIAN EXPORT PROTEIN ALY
FILE REFERENCE: 55047 (70207)
CURRENT APPLICATION NUMBER: US/09/945,248B
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/229,765
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6-His tag
US-09-945-248B-3

Query Match 100.0%; Score 48; DB 3; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 39

US-09-997-623-41
; Sequence 41, Application US/09997623
; Publication No. US20030018175A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us410 - protein C
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US/09/997,623
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide tag
US-09-997-623-41

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 40

US-09-978-917A-41
; Sequence 41, Application US/0978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us310 - protein C
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US/09/978,917A
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide tag
US-09-978-917A-41

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 41

US-09-948-391A-43
; Sequence 43, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase

; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: six histidine
; OTHER INFORMATION: residue tag at amino terminus
US-09-948-391A-43

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 42

US-09-989-981A-11
; Sequence 11, Application US/0989981A
; Publication No. US20030049730A1
; GENERAL INFORMATION:
; APPLICANT: Hobbs, Helen H.
; APPLICANT: Shan, Bei
; APPLICANT: Barnes, Robert
; APPLICANT: Tian, Hui
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use
; FILE REFERENCE: 018781-007320US
; CURRENT APPLICATION NUMBER: US/09/989,981A
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/252,235
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/253,645
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6-His epitope
; OTHER INFORMATION: tag
US-09-989-981A-11

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 43

US-09-948-391A-43
; Sequence 43, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:

RESULT 43
US-09-904-1968-9
Sequence 9, Application US/099041968
Publication No. US20030064922A1
GENERAL INFORMATION:
APPLICANT: NISSEN, TORBEN LAUESGAARD
APPLICANT: ANDERSEN, KIM VILBOUR
APPLICANT: HANSEN, CHRISTIAN KARSTEN
APPLICANT: MIKKELSEN, JAN MOLLER
TITLE OF INVENTION: G-CSF CONJUGATES
FILE REFERENCE: 31-000700US
CURRENT APPLICATION NUMBER: US/09/904,1968
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/760,008
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/176,376
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/189,506
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/215,644
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DK PA 2000 00024
PRIOR FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: DK PA 2000 00341
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: DK PA 2000 00943
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-904-1968-9

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 44
US-09-911-569-106
Sequence 106, Application US/09911569
Publication No. US20030069173A1
GENERAL INFORMATION:
APPLICANT: HAWLEY-NELSON, PAMELA
LAN, JIANQING
SHIH, POJEN
JESSE, JOEL A.
SCHIFFERLI, KEVIN P.
GEBREYERU, GULIAT
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5170 MANHATTAN CIRCLE, SUITE 201
CITY: BOULDER
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,569
FILING DATE: 23-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/039,780
FILING DATE: 16-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 32-95D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-09-911-569-106

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 45
US-09-922-226-43
Sequence 43, Application US/09922226
Publication No. US20030077664A1
GENERAL INFORMATION:
APPLICANT: Zhao, Yi
APPLICANT: Thacher, Scott M.
APPLICANT: Xiaoj, Jia-Hao
APPLICANT: Kusari, Jyotirmoy
APPLICANT: Chandraratna, Roshantha A.
TITLE OF INVENTION: Methods of Screening For Compounds That
Modulate Hormone Receptor Activity
FILE REFERENCE: P-AR 4681
CURRENT APPLICATION NUMBER: US/09/922,226
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/284,797
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-922-226-43

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 46
US-09-906-311C-15

```

Sequence 15, Application US/09906311C
Publication No. US20030087827A1
GENERAL INFORMATION:
APPLICANT: Lindberg, Iris
APPLICANT: Cameron, Angus
APPLICANT: Appel, Jon
APPLICANT: Houghten, Richard
TITLE OF INVENTION: Inhibiting Furin With Polybasic Peptides
FILE REFERENCE: 01M36 Lindberg
CURRENT APPLICATION NUMBER: US/09/906,311C
CURRENT FILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.0, WordPerfect version 8
SEQ ID NO 15
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: De novo designed peptide
US-09-906-311C-15

```

Query Match	100.0%	Score 48:	DB 3:	length 6;
Best Local Similarity	100.0%	Pred. NO.	1.7e+06;	
Best Match	6;	Conservative	0;	Mismatches 0; Gaps 0;

QY	1	HHHHHH	6
Db	1	HHHHHH	6

```

RESULT 47
US-09-782-587B-12
; Sequence 12, Application US/09782587B
; Publication No. US2003009638A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: BORNHAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide tag
; US-09-782-587B-12

```

Query Match	100.0%	Score 48	DB 3	Length 6
Similarity	100.0%	Pred. NO.	1.7e+06	
Best Local	0	Matches	6	Conservative
Matches	0	Mismatches	0	Indels
				Gaps 0

QY	1	HHHHHH	6
Db	1	HHHHHH	6

```

RESULT 48
US-09-802-154-22
; Sequence 22, Application US/09802154
; Publication No. US20030105302A1
; GENERAL INFORMATION:

```

```

1  APPLICANT: Itoh, No. US20030105302A1uyuk1
2  APPLICANT: Kevaneugh, W. Michael
3  TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
4  TITLE OF INVENTION: PRODUCTS
5  FILE REFERENCE: PP-17149, 001/201130, 409
6  CURRENT APPLICATION NUMBER: US/09/802,154
7  CURRENT FILING DATE: 2001-03-07
8  NUMBER OF SEQ ID NOS: 46
9  SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 22
11 LENGTH: 6
12 TYPE: PRT
13 ORGANISM: Artificial Sequence
14 FEATURE:
15 OTHER INFORMATION: His6 tag
16 US-09-802-154-22

```

Query Match	100.0%	Score 48	DB 3	length 6
Similarity	100.0%	Pred. No.	1.7e+06	
Best Local				
Matches	6	Conservative	0	Indels 0
		Mismatches	0	Gaps 0

QY	1	6
Db	1	6

```

1      RESULT 49
2      US-09-961-400-43
3      ; Sequence 43, Application US/09961400
4      ; Publication No. US20030124131A1
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: RYBAK, SUSANNA M.
9      ; APPLICANT: GOLDBERG, DAVID M.
10     ; APPLICANT: NEMTON, DIANNE L.
11     ;
12     ; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
13     ; TITLE OF INVENTION: CELLS
14     ;
15     ; FILE REFERENCE: 018733/1059
16     ;
17     ; CURRENT APPLICATION NUMBER: US/09/961,400
18     ; CURRENT FILING DATE: 2001-09-25
19     ;
20     ; PRIOR APPLICATION NUMBER: 09/622,613
21     ;
22     ; PRIOR FILING DATE: 2000-08-17
23     ;
24     ; PRIOR APPLICATION NUMBER: PCT/US99/06641
25     ; PRIOR FILING DATE: 1999-03-26
26     ; PRIOR APPLICATION NUMBER: 60/079,751
27     ; PRIOR FILING DATE: 1998-03-26
28     ;
29     ; NUMBER OF SEQ ID NOS: 43
30     ;
31     ; SOFTWARE: PatentIn Ver. 2.1
32     ;
33     ; SEQ ID NO 43
34     ;
35     ; LENGTH: 6
36     ;
37     ; TYPE: PRT
38     ;
39     ; ORGANISM: Artificial Sequence
40     ;
41     ; FEATURE:
42     ;
43     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
44     ;
45     ; OTHER INFORMATION: 6X His tag
46     ;
47     US-09-961-400-43

```

Query Match	100.0%	Pred. 48;	DB 3;	Length 6;
Best Local Similarity	100.0%	Pred. No. 1.7e+06;		
Matches 6; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	HHHHH	6
Db	1	HHHHH	6

RESULT 50
US-09-932-165-1480
Sequence 1480, Application US/09932165
Publication NO. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-BUD, PIA M.
APPLICANT: FARIS, MARY

APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: APAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOVITS, AVA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 832H3 AND CATP2E1 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 5158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1480
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6-His tag
US-09-932-165-1480

Query Match 100.0%; Score 48; DB 3; Length 6;
Best local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHHHHH 6
Db 1 HHHHHH 6

Search completed: March 21, 2006, 11:12:34
Job time : 178 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:09:51 ; Search time 23 Seconds
(without alignments)
7.467 Million cell updates/sec

Title: US-10-719-523-5

Perfect score: 48

Sequence: 1 HHHHHH 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 2862289 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA_New:*

1: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep:*

2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*

3: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*

4: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep:*

5: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep:*

6: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*

7: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pep:*

8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	6	US-10-512-184-46	Sequence 46, Appl
2	48	100.0	6	US-10-967-671-18	Sequence 18, Appl
3	48	100.0	6	US-10-966-648-29	Sequence 29, Appl
4	48	100.0	6	US-10-497-767-5	Sequence 5, Appl
5	48	100.0	6	US-10-983-174-1	Sequence 1, Appl
6	48	100.0	6	US-10-475-204-28	Sequence 28, Appl
7	48	100.0	6	US-10-957-351-357	Sequence 357, Appl
8	48	100.0	6	US-10-895-064-27	Sequence 27, Appl
9	48	100.0	6	US-10-950-747-12	Sequence 12, Appl
10	48	100.0	6	US-10-989-767A-698	Sequence 698, App
11	48	100.0	6	US-10-903-612B-120	Sequence 120, App
12	48	100.0	6	US-10-857-435A-622	Sequence 622, App
13	48	100.0	6	US-10-861-105-2	Sequence 2, Appl
14	48	100.0	6	US-10-968-629-13	Sequence 13, Appl
15	48	100.0	6	US-10-498-665-72	Sequence 62, Appl
16	48	100.0	6	US-11-085-864-6	Sequence 6, Appl
17	48	100.0	6	US-11-158-848-35	Sequence 35, Appl
18	48	100.0	6	US-11-040-159-21	Sequence 21, Appl
19	48	100.0	6	US-11-040-114-9	Sequence 9, Appl
20	48	100.0	6	US-11-073-605-16	Sequence 16, Appl
21	48	100.0	6	US-11-102-428-8	Sequence 8, Appl
22	48	100.0	6	US-11-127-004-4	Sequence 4, Appl
23	48	100.0	6	US-11-000-365-46	Sequence 46, Appl
24	48	100.0	6	US-11-032-794-46	Sequence 46, Appl
25	48	100.0	6	US-11-097-749-40	Sequence 40, Appl

26	48	100.0	6	US-11-006-031-20	Sequence 20, Appl
27	48	100.0	6	US-11-073-927-6	Sequence 6, Appl
28	48	100.0	6	US-11-114-922-91	Sequence 91, Appl
29	48	100.0	6	US-11-037-243-149	Sequence 149, App
30	48	100.0	6	US-11-033-039-357	Sequence 357, App
31	48	100.0	6	US-11-047-383-32	Sequence 32, Appl
32	48	100.0	6	US-11-124-635-14	Sequence 14, Appl
33	48	100.0	6	US-11-155-446-3	Sequence 3, Appl
34	48	100.0	6	US-11-202-516-22	Sequence 22, Appl
35	48	100.0	6	US-11-008-570-129	Sequence 129, App
36	48	100.0	6	US-11-056-182-19	Sequence 19, Appl
37	48	100.0	6	US-11-153-086-5	Sequence 5, Appl
38	48	100.0	6	US-11-121-612-400	Sequence 400, App
39	48	100.0	6	US-11-131-744-9	Sequence 9, Appl
40	48	100.0	6	US-11-194-110-20	Sequence 20, Appl
41	48	100.0	6	US-11-051-178A-21	Sequence 21, Appl
42	48	100.0	6	US-11-129-741-27	Sequence 27, Appl
43	48	100.0	6	US-11-151-762-1	Sequence 1, Appl
44	48	100.0	6	US-11-108-088-71	Sequence 71, Appl
45	48	100.0	6	US-11-123-893-18	Sequence 18, Appl
46	48	100.0	6	US-11-179-363-29	Sequence 29, Appl
47	48	100.0	7	US-11-108-001-13	Sequence 13, Appl
48	48	100.0	7	US-11-222-451-21	Sequence 21, Appl
49	48	100.0	8	US-10-950-747-13	Sequence 13, Appl
50	48	100.0	8	US-10-498-665-73	Sequence 73, Appl
51	48	100.0	8	US-11-158-848-36	Sequence 36, App
52	48	100.0	8	US-11-032-773-936	Sequence 936, App
53	48	100.0	8	US-11-192-341-20	Sequence 20, Appl
54	48	100.0	9	US-10-956-755A-100	Sequence 100, App
55	48	100.0	9	US-11-119-212-27	Sequence 27, Appl
56	48	100.0	9	US-11-119-212-29	Sequence 29, Appl
57	48	100.0	10	US-11-157-360-9	Sequence 9, Appl
58	48	100.0	10	US-11-150-533-51	Sequence 51, Appl
59	48	100.0	10	US-11-187-622-31	Sequence 31, Appl
60	48	100.0	11	US-10-508-893-1	Sequence 1, Appl
61	48	100.0	11	US-11-154-852-1	Sequence 1, Appl
62	48	100.0	12	US-11-179-363-30	Sequence 30, Appl
63	48	100.0	14	US-11-192-341-10	Sequence 10, Appl
64	48	100.0	15	US-10-967-671-8	Sequence 8, Appl
65	48	100.0	15	US-10-903-612B-97	Sequence 97, Appl
66	48	100.0	15	US-11-047-383-8	Sequence 8, Appl
67	48	100.0	15	US-11-237-597-22	Sequence 22, Appl
68	48	100.0	15	US-11-073-942-9	Sequence 9, Appl
69	48	100.0	16	US-10-903-612B-104	Sequence 104, App
70	48	100.0	16	US-11-082-544-23	Sequence 23, Appl
71	48	100.0	16	US-11-195-739-13	Sequence 13, Appl
72	48	100.0	17	US-11-065-943-40	Sequence 40, Appl
73	48	100.0	18	US-10-914-165-45	Sequence 45, Appl
74	48	100.0	18	US-10-903-612B-98	Sequence 98, Appl
75	48	100.0	18	US-10-903-612B-99	Sequence 99, Appl
76	48	100.0	18	US-10-903-612B-101	Sequence 101, App
77	48	100.0	18	US-10-903-612B-102	Sequence 102, App
78	48	100.0	18	US-10-903-612B-103	Sequence 103, App
79	48	100.0	18	US-11-137-671-17	Sequence 17, Appl
80	48	100.0	18	US-11-197-721-55	Sequence 55, Appl
81	48	100.0	18	US-11-155-446-4	Sequence 4, Appl
82	48	100.0	19	US-10-903-612B-105	Sequence 105, App
83	48	100.0	19	US-10-903-612B-106	Sequence 106, App
84	48	100.0	19	US-10-903-612B-107	Sequence 107, App
85	48	100.0	19	US-10-903-612B-108	Sequence 108, App
86	48	100.0	19	US-10-903-612B-109	Sequence 109, App
87	48	100.0	19	US-11-137-671-12	Sequence 12, Appl
88	48	100.0	20	US-10-967-671-7	Sequence 7, Appl
89	48	100.0	20	US-10-850-207-5	Sequence 5, Appl
90	48	100.0	20	US-10-503-939-14	Sequence 14, Appl
91	48	100.0	20	US-11-053-187-19	Sequence 19, Appl
92	48	100.0	20	US-11-047-383-7	Sequence 7, Appl
93	48	100.0	21	US-11-185-111-41	Sequence 41, Appl
94	48	100.0	21	US-11-148-108-51	Sequence 51, Appl
95	48	100.0	21	US-11-094-071-31	Sequence 31, Appl
96	48	100.0	21	US-11-201-347-25	Sequence 25, Appl
97	48	100.0	22	US-11-019-027-37	Sequence 37, Appl
98	48	100.0	23	US-11-225-709-37	Sequence 37, Appl

99	48	100.0	24	6	US-10-985-321A-15	Sequence 15, Appl	172	48	100.0	129	7	US-11-064-774A-111	Sequence 111, App
100	48	100.0	24	7	US-11-224-268-2	Sequence 2, Appl1	173	48	100.0	129	7	US-11-064-774A-113	Sequence 113, App
101	48	100.0	24	7	US-11-225-709-39	Sequence 39, Appl	174	48	100.0	129	7	US-11-096-568A-956	Sequence 956, App
102	48	100.0	24	7	US-11-174-467-9	Sequence 9, Appl1	175	48	100.0	133	7	US-11-088-008-1	Sequence 1, Appl1
103	48	100.0	25	7	US-11-096-051-38	Sequence 38, Appl	176	48	100.0	133	7	US-11-174-784-1	Sequence 1, Appl1
104	48	100.0	25	7	US-11-189-832-5	Sequence 5, Appl1	177	48	100.0	139	7	US-11-085-792-4	Sequence 4, Appl1
105	48	100.0	25	7	US-11-191-024-5	Sequence 5, Appl1	178	48	100.0	139	7	US-11-096-568A-7287	Sequence 7287, Ap
106	48	100.0	25	7	US-11-247-356-5	Sequence 5, Appl1	179	48	100.0	140	7	US-11-082-544-60	Sequence 60, Appl
107	48	100.0	26	6	US-10-850-207-6	Sequence 6, Appl1	180	48	100.0	143	7	US-11-116-184-166	Sequence 166, App
108	48	100.0	27	6	US-11-086-482-2	Sequence 2, Appl1	181	48	100.0	143	7	US-11-102-883-12	Sequence 12, App
109	48	100.0	29	6	US-10-850-207-7	Sequence 7, Appl1	182	48	100.0	144	7	US-11-143-947A-3	Sequence 3, Appl1
110	48	100.0	29	7	US-11-157-360-17	Sequence 17, Appl	183	48	100.0	144	7	US-11-143-947A-3	Sequence 3, Appl1
111	48	100.0	33	6	US-10-809-208-22	Sequence 22, Appl	184	48	100.0	149	7	US-11-156-909-19	Sequence 19, Appl
112	48	100.0	33	7	US-11-122-795-6	Sequence 6, Appl1	185	48	100.0	149	7	US-11-156-909-23	Sequence 23, Appl
113	48	100.0	33	7	US-11-122-795-7	Sequence 7, Appl1	186	48	100.0	149	7	US-11-156-909-27	Sequence 27, Appl
114	48	100.0	33	7	US-11-218-880-22	Sequence 22, Appl	187	48	100.0	149	7	US-11-156-909-31	Sequence 31, Appl
115	48	100.0	37	7	US-11-219-282-15	Sequence 15, Appl	188	48	100.0	149	7	US-11-156-909-35	Sequence 35, Appl
116	48	100.0	38	7	US-11-122-795-12	Sequence 12, Appl	189	48	100.0	149	7	US-11-156-909-39	Sequence 39, Appl
117	48	100.0	41	7	US-11-131-744-5	Sequence 5, Appl1	190	48	100.0	149	7	US-11-267-310-67	Sequence 67, Appl
118	48	100.0	41	7	US-11-121-612-296	Sequence 296, App	191	48	100.0	150	7	US-11-267-310-9	Sequence 9, Appl
119	48	100.0	44	6	US-10-816-768-91	Sequence 91, Appl1	192	48	100.0	152	7	US-11-075-047A-107	Sequence 107, App
120	48	100.0	47	6	US-11-151-598-5	Sequence 5, Appl1	193	48	100.0	152	7	US-11-267-310-7	Sequence 7, Appl1
121	48	100.0	49	6	US-10-968-629-26	Sequence 26, Appl	194	48	100.0	153	7	US-11-267-310-5	Sequence 5, Appl1
122	48	100.0	57	6	US-10-968-629-23	Sequence 23, Appl	195	48	100.0	153	7	US-10-952-535A-17	Sequence 17, Appl
123	48	100.0	57	6	US-10-968-629-29	Sequence 29, Appl	196	48	100.0	155	6	US-10-952-535A-17	Sequence 17, Appl
124	48	100.0	64	6	US-10-816-768-108	Sequence 108, App	197	48	100.0	160	7	US-11-143-947A-1	Sequence 1, Appl1
125	48	100.0	68	6	US-10-968-629-25	Sequence 25, Appl	198	48	100.0	160	7	US-11-143-947A-1	Sequence 1, Appl1
126	48	100.0	73	6	US-10-968-629-30	Sequence 30, Appl	199	48	100.0	161	6	US-10-623-155-423	Sequence 423, App
127	48	100.0	80	7	US-10-623-155-361	Sequence 361, App	200	48	100.0	164	7	US-11-108-001-2	Sequence 2, Appl1
128	48	100.0	80	7	US-11-030-313-1	Sequence 1, Appl1	201	48	100.0	168	7	US-11-075-047A-109	Sequence 109, App
129	48	100.0	82	6	US-10-968-629-27	Sequence 27, Appl	202	48	100.0	170	6	US-10-990-627-6	Sequence 6, Appl1
130	48	100.0	89	6	US-10-816-768-98	Sequence 98, Appl	203	48	100.0	172	7	US-11-102-883-18	Sequence 18, Appl
131	48	100.0	91	7	US-11-131-744-1	Sequence 1, Appl1	204	48	100.0	173	7	US-11-156-909-21	Sequence 21, Appl
132	48	100.0	92	6	US-10-968-629-31	Sequence 31, Appl	205	48	100.0	173	7	US-11-156-909-17	Sequence 17, Appl
133	48	100.0	95	7	US-11-119-212-11	Sequence 11, Appl	206	48	100.0	173	7	US-11-156-909-29	Sequence 29, Appl
134	48	100.0	96	7	US-10-925-366A-222	Sequence 222, App	207	48	100.0	173	7	US-11-156-909-33	Sequence 33, Appl
135	48	100.0	96	6	US-10-952-535A-15	Sequence 15, Appl	208	48	100.0	173	7	US-11-156-909-37	Sequence 37, Appl
136	48	100.0	98	6	US-10-968-629-28	Sequence 28, App	209	48	100.0	173	7	US-11-143-947A-8	Sequence 8, Appl1
137	48	100.0	109	6	US-10-968-629-28	Sequence 28, App	210	48	100.0	173	7	US-11-143-947A-8	Sequence 8, Appl1
138	48	100.0	111	6	US-10-816-768-96	Sequence 96, Appl	211	48	100.0	174	7	US-11-156-909-25	Sequence 25, Appl
139	48	100.0	113	6	US-10-968-629-32	Sequence 32, Appl	212	48	100.0	177	7	US-11-131-744-3	Sequence 3, Appl1
140	48	100.0	123	6	US-10-952-535A-16	Sequence 32, Appl	213	48	100.0	180	7	US-11-096-568A-21170	Sequence 21170, A
141	48	100.0	126	7	US-11-064-774A-43	Sequence 43, Appl	214	48	100.0	180	7	US-11-143-947A-2	Sequence 2, Appl1
142	48	100.0	126	7	US-11-064-774A-53	Sequence 53, Appl	215	48	100.0	180	7	US-11-143-947A-2	Sequence 2, Appl1
143	48	100.0	126	7	US-11-064-774A-55	Sequence 55, Appl	216	48	100.0	181	7	US-11-143-947A-4	Sequence 4, Appl1
144	48	100.0	126	7	US-11-064-774A-57	Sequence 57, Appl	217	48	100.0	181	7	US-11-143-947A-4	Sequence 4, Appl1
145	48	100.0	126	7	US-11-064-774A-61	Sequence 61, Appl	218	48	100.0	185	7	US-11-096-568A-22116	Sequence 22116, A
146	48	100.0	126	7	US-11-064-774A-63	Sequence 63, Appl	219	48	100.0	192	7	US-11-096-568A-7286	Sequence 7286, Ap
147	48	100.0	126	7	US-11-064-774A-65	Sequence 65, Appl	220	48	100.0	194	7	US-11-096-568A-22115	Sequence 22115, A
148	48	100.0	127	7	US-11-064-774A-47	Sequence 47, Appl	221	48	100.0	203	6	US-10-816-768-100	Sequence 100, App
149	48	100.0	127	7	US-11-064-774A-83	Sequence 83, Appl	222	48	100.0	204	7	US-11-087-099-12123	Sequence 12123, A
150	48	100.0	127	7	US-11-064-774A-85	Sequence 85, Appl	223	48	100.0	209	6	US-10-518-701-6	Sequence 6, Appl1
151	48	100.0	127	7	US-11-064-774A-87	Sequence 87, Appl	224	48	100.0	212	7	US-11-096-568A-16894	Sequence 16894, A
152	48	100.0	127	7	US-11-064-774A-89	Sequence 89, Appl	225	48	100.0	215	7	US-11-119-212-9	Sequence 9, Appl1
153	48	100.0	127	7	US-11-064-774A-91	Sequence 91, Appl	226	48	100.0	220	7	US-11-222-451-10	Sequence 10, Appl
154	48	100.0	127	7	US-11-064-774A-93	Sequence 93, Appl	227	48	100.0	221	7	US-11-194-246-339	Sequence 339, App
155	48	100.0	127	7	US-11-064-774A-95	Sequence 95, Appl	228	48	100.0	224	7	US-11-096-568A-16893	Sequence 16893, A
156	48	100.0	127	7	US-11-064-774A-97	Sequence 97, Appl	229	48	100.0	225	7	US-11-151-598-7	Sequence 7, Appl1
157	48	100.0	127	7	US-11-176-525-2	Sequence 2, Appl1	230	48	100.0	225	7	US-11-151-598-8	Sequence 8, Appl1
158	48	100.0	128	7	US-11-064-774A-45	Sequence 45, Appl	231	48	100.0	227	7	US-11-151-598-8	Sequence 8, Appl1
159	48	100.0	128	7	US-11-064-774A-67	Sequence 67, Appl	232	48	100.0	227	7	US-11-096-568A-21272	Sequence 21272, A
160	48	100.0	128	7	US-11-064-774A-69	Sequence 69, Appl	233	48	100.0	230	7	US-11-222-451-6	Sequence 6, Appl1
161	48	100.0	128	7	US-11-064-774A-71	Sequence 71, Appl	234	48	100.0	231	7	US-11-201-519-28	Sequence 28, Appl
162	48	100.0	128	7	US-11-064-774A-73	Sequence 73, Appl	235	48	100.0	232	7	US-11-143-947A-5	Sequence 5, Appl1
163	48	100.0	128	7	US-11-064-774A-75	Sequence 75, Appl	236	48	100.0	232	7	US-11-143-947A-5	Sequence 5, Appl1
164	48	100.0	128	7	US-11-064-774A-79	Sequence 79, Appl	237	48	100.0	233	6	US-10-949-720-388	Sequence 388, App
165	48	100.0	129	7	US-11-064-774A-49	Sequence 49, Appl	238	48	100.0	239	7	US-11-096-568A-7444	Sequence 7444, Ap
166	48	100.0	129	7	US-11-064-774A-99	Sequence 99, Appl	239	48	100.0	239	7	US-11-096-568A-16892	Sequence 16892, A
167	48	100.0	129	7	US-11-064-774A-101	Sequence 101, App	240	48	100.0	243	7	US-11-108-1172-1122	Sequence 1122, Ap
168	48	100.0	129	7	US-11-064-774A-103	Sequence 103, App	241	48	100.0	247	7	US-11-199-915-3	Sequence 3, Appl1
169	48	100.0	129	7	US-11-064-774A-105	Sequence 105, App	242	48	100.0	249	6	US-10-909-957-2	Sequence 2, Appl1
170	48	100.0	129	7	US-11-064-774A-107	Sequence 107, App	243	48	100.0	249	7	US-11-201-825-7	Sequence 7, Appl1
171	48	100.0	129	7	US-11-064-774A-109	Sequence 109, App	244	48	100.0	249	7	US-11-201-825-24	Sequence 24, Appl

245	48	100.0	249	7	US-11-096-568A-21271	Sequence 21271, A	318	48	100.0	315	7	US-11-198-794-91	Sequence 91, Appl
246	48	100.0	252	7	US-11-096-568A-12561	Sequence 12561, A	319	48	100.0	315	7	US-11-198-657-91	Sequence 2, Appl
247	48	100.0	254	6	US-10-714-887-126	Sequence 126, App	320	48	100.0	317	6	US-10-000-997-2	Sequence 2, Appl
248	48	100.0	255	7	US-11-197-488-37	Sequence 37, Appl	321	48	100.0	317	6	US-10-000-997-4	Sequence 4, Appl
249	48	100.0	256	7	US-11-124-635-7	Sequence 7, Appl	322	48	100.0	317	6	US-10-000-997-6	Sequence 8, Appl
250	48	100.0	258	7	US-11-201-825-8	Sequence 8, Appl	323	48	100.0	317	6	US-10-000-997-8	Sequence 8, Appl
251	48	100.0	258	7	US-11-201-825-25	Sequence 25, Appl	324	48	100.0	319	7	US-11-032-773-955	Sequence 955, App
252	48	100.0	260	7	US-11-197-488-23	Sequence 23, Appl	325	48	100.0	319	7	US-11-096-568A-19888	Sequence 19888, A
253	48	100.0	260	7	US-11-197-488-39	Sequence 39, Appl	326	48	100.0	320	7	US-11-096-568A-6440	Sequence 6440, App
254	48	100.0	260	7	US-11-096-568A-12560	Sequence 12560, A	327	48	100.0	322	6	US-10-330-773-977	Sequence 977, App
255	48	100.0	261	7	US-11-087-099-11099	Sequence 11099, A	328	48	100.0	324	7	US-11-119-212-15	Sequence 15, Appl
256	48	100.0	262	7	US-11-201-825-9	Sequence 9, Appl	329	48	100.0	324	7	US-11-196-618-16	Sequence 16, Appl
257	48	100.0	262	7	US-11-199-820-4	Sequence 4, Appl	330	48	100.0	334	7	US-11-196-618-18	Sequence 18, Appl
258	48	100.0	264	7	US-11-176-525-1	Sequence 1, Appl	331	48	100.0	336	7	US-11-119-212-19	Sequence 19, Appl
259	48	100.0	267	6	US-10-623-155-352	Sequence 352, App	332	48	100.0	336	7	US-11-096-568A-11596	Sequence 11596, A
260	48	100.0	267	6	US-10-503-939-15	Sequence 15, Appl	333	48	100.0	327	6	US-10-055-877-183	Sequence 183, App
261	48	100.0	267	6	US-10-503-939-16	Sequence 16, Appl	334	48	100.0	328	6	US-10-714-887-350	Sequence 350, App
262	48	100.0	267	6	US-10-503-939-17	Sequence 17, Appl	335	48	100.0	328	6	US-11-096-568A-5465	Sequence 5465, App
263	48	100.0	267	6	US-10-503-939-18	Sequence 18, Appl	336	48	100.0	329	7	US-11-087-099-2753	Sequence 2753, App
264	48	100.0	267	6	US-10-503-939-19	Sequence 19, Appl	337	48	100.0	331	7	US-11-201-519-4	Sequence 4, Appl
265	48	100.0	267	6	US-10-503-939-20	Sequence 20, Appl	338	48	100.0	331	7	US-11-087-099-6481	Sequence 6481, App
266	48	100.0	267	6	US-10-503-939-21	Sequence 21, Appl	339	48	100.0	331	7	US-11-096-568A-11595	Sequence 11595, A
267	48	100.0	267	6	US-10-503-939-22	Sequence 22, Appl	340	48	100.0	332	6	US-10-949-720-405	Sequence 405, App
268	48	100.0	267	6	US-10-503-939-23	Sequence 23, Appl	341	48	100.0	333	7	US-11-096-568A-6439	Sequence 6439, App
269	48	100.0	267	6	US-11-151-598-2	Sequence 2, Appl	342	48	100.0	334	6	US-10-514-057-6	Sequence 6, Appl
270	48	100.0	267	7	US-11-179-363-3	Sequence 3, Appl	343	48	100.0	334	6	US-10-714-887-46	Sequence 46, Appl
271	48	100.0	272	7	US-11-119-212-31	Sequence 31, Appl	344	48	100.0	334	6	US-11-096-568A-5464	Sequence 5464, App
272	48	100.0	273	7	US-11-131-744-6	Sequence 6, Appl	345	48	100.0	339	7	US-11-096-568A-28931	Sequence 28931, A
273	48	100.0	274	7	US-11-102-883-34	Sequence 34, Appl	346	48	100.0	339	7	US-11-096-568A-11981	Sequence 11981, A
274	48	100.0	276	7	US-11-038-901-19	Sequence 19, Appl	347	48	100.0	341	7	US-11-087-099-11420	Sequence 11420, A
275	48	100.0	277	6	US-10-996-0078-13	Sequence 13, Appl	348	48	100.0	346	7	US-11-108-172-1085	Sequence 1085, App
276	48	100.0	277	6	US-10-996-0078-14	Sequence 14, Appl	349	48	100.0	346	7	US-11-087-099-9486	Sequence 9486, App
277	48	100.0	277	6	US-10-996-0078-15	Sequence 15, Appl	350	48	100.0	347	7	US-11-102-883-4	Sequence 4, Appl
278	48	100.0	279	7	US-11-096-568A-21270	Sequence 21270, A	351	48	100.0	348	7	US-11-096-568A-11980	Sequence 11980, A
279	48	100.0	285	6	US-10-714-887-304	Sequence 304, App	352	48	100.0	348	6	US-10-055-877-169	Sequence 169, App
280	48	100.0	289	7	US-11-102-883-2	Sequence 2, Appl	353	48	100.0	349	6	US-10-055-877-170	Sequence 170, App
281	48	100.0	290	7	US-11-032-773-957	Sequence 957, App	354	48	100.0	349	6	US-10-055-877-171	Sequence 171, App
282	48	100.0	292	7	US-11-102-883-34	Sequence 34, Appl	355	48	100.0	350	7	US-11-096-568A-32434	Sequence 32434, A
283	48	100.0	293	6	US-10-841-956A-9	Sequence 9, Appl	356	48	100.0	351	7	US-11-096-568A-32434	Sequence 2, Appl
284	48	100.0	294	7	US-11-102-883-30	Sequence 30, Appl	357	48	100.0	353	6	US-10-055-877-30	Sequence 30, Appl
285	48	100.0	295	7	US-11-096-568A-7443	Sequence 7443, App	358	48	100.0	353	6	US-11-096-568A-12556	Sequence 12556, A
286	48	100.0	296	7	US-11-096-051-18	Sequence 18, Appl	359	48	100.0	356	6	US-10-055-877-185	Sequence 184, App
287	48	100.0	298	7	US-11-087-099-10462	Sequence 10462, A	360	48	100.0	356	6	US-10-055-877-185	Sequence 185, App
288	48	100.0	299	6	US-10-623-155-354	Sequence 354, App	361	48	100.0	356	7	US-11-217-137-10	Sequence 10, Appl
289	48	100.0	299	7	US-11-201-519-19	Sequence 19, Appl	362	48	100.0	359	7	US-11-096-568A-28234	Sequence 28234, A
290	48	100.0	300	7	US-11-087-099-2899	Sequence 2899, App	363	48	100.0	362	7	US-11-102-883-8	Sequence 8, Appl
291	48	100.0	309	7	US-11-102-883-6	Sequence 6, Appl	364	48	100.0	363	7	US-11-096-568A-5463	Sequence 5463, App
292	48	100.0	301	7	US-11-116-319-2	Sequence 2, Appl	365	48	100.0	364	7	US-11-087-099-934	Sequence 934, App
293	48	100.0	302	6	US-10-857-435A-615	Sequence 615, App	366	48	100.0	365	7	US-11-096-568A-11594	Sequence 11594, A
294	48	100.0	302	7	US-11-119-212-13	Sequence 13, Appl	367	48	100.0	366	7	US-11-087-099-11191	Sequence 11191, A
295	48	100.0	302	7	US-11-119-212-25	Sequence 25, Appl	368	48	100.0	368	7	US-11-301-519-24	Sequence 24, Appl
296	48	100.0	303	7	US-11-087-099-8877	Sequence 8877, App	369	48	100.0	368	7	US-11-096-568A-32433	Sequence 32433, A
297	48	100.0	304	7	US-11-087-099-7559	Sequence 7559, App	370	48	100.0	369	7	US-11-087-099-8929	Sequence 8929, App
298	48	100.0	304	7	US-11-096-568A-32073	Sequence 32073, A	371	48	100.0	370	7	US-10-623-155-433	Sequence 433, App
299	48	100.0	306	6	US-10-000-997-44	Sequence 44, Appl	372	48	100.0	371	6	US-11-137-671-16	Sequence 16, Appl
300	48	100.0	306	6	US-11-096-568A-32072	Sequence 32072, A	373	48	100.0	375	7	US-11-096-568A-28233	Sequence 28233, A
301	48	100.0	308	6	US-10-914-573A-1	Sequence 1, Appl	374	48	100.0	376	7	US-11-087-099-6311	Sequence 6311, App
302	48	100.0	308	6	US-10-914-573A-2	Sequence 2, Appl	375	48	100.0	378	7	US-11-201-606-26	Sequence 26, Appl
303	48	100.0	308	6	US-10-914-769-1	Sequence 1, Appl	376	48	100.0	379	7	US-11-096-568A-7314	Sequence 7314, App
304	48	100.0	309	7	US-11-245-053-9	Sequence 9, Appl	377	48	100.0	379	7	US-11-196-019A-7	Sequence 7, Appl
305	48	100.0	308	6	US-10-914-769-2	Sequence 2, Appl	378	48	100.0	382	7	US-11-143-943A-6	Sequence 6, Appl
306	48	100.0	308	7	US-11-046-456-6	Sequence 6, Appl	379	48	100.0	383	7	US-11-143-943A-6	Sequence 6, Appl
307	48	100.0	308	7	US-11-046-456-6	Sequence 6, Appl	380	48	100.0	383	7	US-11-123-893-11	Sequence 11, Appl
308	48	100.0	308	7	US-11-046-456-6	Sequence 6, Appl	381	48	100.0	385	6	US-10-853-533-3	Sequence 3, Appl
309	48	100.0	308	7	US-11-096-568A-14791	Sequence 14791, A	382	48	100.0	387	6	US-10-949-720-419	Sequence 419, App
310	48	100.0	309	7	US-11-096-568A-28932	Sequence 28932, A	383	48	100.0	388	48	100.0	Sequence 4, Appl
311	48	100.0	310	7	US-11-245-053-3	Sequence 3, Appl	384	48	100.0	389	48	100.0	Sequence 23, Appl
312	48	100.0	310	7	US-11-086-482-3	Sequence 8, Appl	385	48	100.0	390	48	100.0	Sequence 25, Appl
313	48	100.0	311	6	US-11-245-053-11	Sequence 11, Appl	386	48	100.0				
314	48	100.0	311	6	US-10-055-877-181	Sequence 181, App	387	48	100.0				
315	48	100.0	312	6	US-10-055-877-182	Sequence 182, App	388	48	100.0				
316	48	100.0	312	6	US-11-245-053-10	Sequence 10, Appl	389	48	100.0				
317	48	100.0	315	7	US-11-096-568A-32071	Sequence 32071, A	390	48	100.0				

391	48	100.0	404	7	US-11-096-568A-19887	Sequence 19887, A	464	48	100.0	614	7	US-11-015-546A-20	Sequence 20, Appl
392	48	100.0	407	6	US-10-996-104A-20	Sequence 20, Appl	465	48	100.0	615	6	US-10-512-184-50	Sequence 50, Appl
393	48	100.0	411	7	US-11-119-212-17	Sequence 17, Appl	466	48	100.0	616	7	US-11-087-099-8299	Sequence 8299, Ap
394	48	100.0	412	7	US-11-168-874-12	Sequence 12, Appl	467	48	100.0	618	6	US-10-512-184-48	Sequence 48, Appl
395	48	100.0	413	7	US-11-119-212-21	Sequence 21, Appl	468	48	100.0	619	7	US-11-087-099-12402	Sequence 12402, A
396	48	100.0	414	7	US-11-096-568A-23357	Sequence 23357, A	469	48	100.0	620	7	US-11-087-099-3888	Sequence 3888, Ap
397	48	100.0	415	6	US-10-980-866-5	Sequence 5, Appl1	470	48	100.0	623	6	US-10-512-184-47	Sequence 5188, Ap
398	48	100.0	416	7	US-11-019-969-3	Sequence 5, Appl1	471	48	100.0	625	6	US-10-512-184-47	Sequence 47, Appl
399	48	100.0	417	7	US-11-196-019A-5	Sequence 5, Appl1	472	48	100.0	626	6	US-10-512-184-49	Sequence 49, Appl
400	48	100.0	418	6	US-10-996-104A-6	Sequence 6, Appl1	473	48	100.0	633	7	US-11-087-099-564	Sequence 564, App
401	48	100.0	419	6	US-11-096-568A-32432	Sequence 32432, A	474	48	100.0	644	7	US-11-087-099-9298	Sequence 9298, Ap
402	48	100.0	423	7	US-10-714-887-122	Sequence 122, App	475	48	100.0	645	7	US-11-067-260-44	Sequence 44, Appl
403	48	100.0	427	6	US-11-096-568A-23356	Sequence 23356, A	476	48	100.0	648	7	US-11-067-260-22	Sequence 28, Appl
404	48	100.0	430	7	US-10-949-720-410	Sequence 410, App	477	48	100.0	651	6	US-10-994-820A-34	Sequence 34, Appl
405	48	100.0	431	6	US-10-949-720-410	Sequence 410, App	478	48	100.0	672	7	US-11-067-260-36	Sequence 36, Appl
406	48	100.0	431	6	US-10-499-246-11	Sequence 11, Appl	479	48	100.0	675	7	US-11-067-260-34	Sequence 34, Appl
407	48	100.0	433	7	US-11-201-519-14	Sequence 14, Appl	480	48	100.0	690	6	US-10-467-962B-101	Sequence 101, App
408	48	100.0	437	6	US-10-860-866-3	Sequence 3, Appl1	481	48	100.0	684	7	US-11-096-568A-23369	Sequence 23369, A
409	48	100.0	437	6	US-11-019-969-3	Sequence 3, Appl1	482	48	100.0	685	7	US-11-169-041-194	Sequence 194, App
410	48	100.0	437	7	US-11-196-019A-3	Sequence 2, Appl1	483	48	100.0	710	7	US-11-126-022-34	Sequence 34, Appl
411	48	100.0	440	6	US-10-933-115-2	Sequence 2, Appl1	484	48	100.0	717	7	US-11-201-519-16	Sequence 16, Appl
412	48	100.0	440	7	US-11-131-744-7	Sequence 7, Appl1	485	48	100.0	725	6	US-11-121-438-10	Sequence 10, Appl
413	48	100.0	444	7	US-11-143-947A-7	Sequence 7, Appl1	486	48	100.0	725	6	US-10-499-290-3	Sequence 3, Appl1
414	48	100.0	446	7	US-11-143-947A-7	Sequence 7, Appl1	487	48	100.0	729	7	US-11-201-519-2	Sequence 2, Appl1
415	48	100.0	447	7	US-11-108-172-1121	Sequence 1121, Ap	488	48	100.0	729	7	US-11-222-451-12	Sequence 12, Appl
416	48	100.0	447	7	US-11-096-568A-30971	Sequence 30971, A	489	48	100.0	738	6	US-10-523-038-39	Sequence 39, Appl
417	48	100.0	449	7	US-11-169-041-138	Sequence 138, App	490	48	100.0	751	7	US-11-067-260-40	Sequence 40, Appl
418	48	100.0	449	7	US-11-234-786-617	Sequence 617, App	491	48	100.0	751	7	US-11-067-260-48	Sequence 48, Appl
419	48	100.0	460	6	US-10-996-104A-22	Sequence 22, Appl	492	48	100.0	753	7	US-11-013-247A-35	Sequence 35, Appl
420	48	100.0	465	7	US-11-096-568A-32100	Sequence 32100, A	493	48	100.0	766	6	US-10-821-234-1691	Sequence 1691, Ap
421	48	100.0	469	7	US-11-087-099-321	Sequence 321, App	494	48	100.0	766	7	US-11-189-391-21	Sequence 21, Appl
422	48	100.0	469	7	US-11-087-099-6164	Sequence 6164, Ap	495	48	100.0	800	7	US-11-217-137-11	Sequence 11, Appl
423	48	100.0	475	7	US-11-096-568A-23355	Sequence 23355, A	496	48	100.0	802	7	US-11-201-519-10	Sequence 10, Appl
424	48	100.0	475	7	US-11-096-568A-32099	Sequence 32099, A	497	48	100.0	806	7	US-11-067-260-38	Sequence 38, Appl
425	48	100.0	484	6	US-11-087-099-4840	Sequence 4840, Ap	498	48	100.0	806	7	US-11-067-260-42	Sequence 42, Appl
426	48	100.0	484	6	US-10-980-866-1	Sequence 1, Appl1	499	48	100.0	811	6	US-11-038-284-42	Sequence 42, Appl
427	48	100.0	484	7	US-11-019-869-1	Sequence 1, Appl1	500	48	100.0	811	6	US-11-038-284-42	Sequence 42, Appl
428	48	100.0	484	7	US-11-196-019A-1	Sequence 1, Appl1	501	48	100.0	826	7	US-11-201-519-12	Sequence 12, Appl
429	48	100.0	487	7	US-11-179-363-11	Sequence 11, Appl1	502	48	100.0	827	7	US-11-096-051-20	Sequence 20, Appl
430	48	100.0	489	6	US-10-835-475-11	Sequence 11, Appl	503	48	100.0	827	7	US-11-077-550-159	Sequence 159, App
431	48	100.0	490	7	US-11-065-716-16	Sequence 16, Appl	504	48	100.0	831	6	US-10-623-155-430	Sequence 430, Appl
432	48	100.0	490	7	US-11-087-099-9408	Sequence 9408, Ap	505	48	100.0	884	7	US-11-201-606-34	Sequence 34, Appl
433	48	100.0	492	7	US-11-197-488-27	Sequence 27, Appl	506	48	100.0	887	7	US-11-077-550-161	Sequence 161, App
434	48	100.0	494	7	US-11-087-099-3900	Sequence 3900, Ap	507	48	100.0	920	6	US-10-623-155-357	Sequence 357, App
435	48	100.0	494	7	US-11-087-099-4874	Sequence 4874, Ap	508	48	100.0	926	7	US-11-201-606-33	Sequence 30, Appl
436	48	100.0	496	7	US-11-096-568A-29371	Sequence 29371, A	509	48	100.0	932	7	US-11-087-099-8167	Sequence 8167, Ap
437	48	100.0	510	7	US-11-096-568A-28930	Sequence 28930, A	510	48	100.0	958	7	US-11-087-099-11814	Sequence 11814, A
438	48	100.0	514	6	US-11-179-363-2	Sequence 2, Appl1	511	48	100.0	966	7	US-11-108-172-1087	Sequence 1087, Ap
439	48	100.0	514	6	US-10-835-475-2	Sequence 2, Appl1	512	48	100.0	1002	7	US-11-201-606-34	Sequence 34, Appl
440	48	100.0	530	7	US-11-207-078-603	Sequence 603, App	513	48	100.0	1002	7	US-11-201-606-25	Sequence 25, Appl
441	48	100.0	543	6	US-10-495-664-3	Sequence 3, Appl1	514	48	100.0	1010	6	US-10-959-611-2	Sequence 2, Appl1
442	48	100.0	545	7	US-11-096-568A-32098	Sequence 32098, A	515	48	100.0	1164	7	US-11-207-078-611	Sequence 611, App
443	48	100.0	548	7	US-11-096-568A-29370	Sequence 29370, A	516	48	100.0	1168	6	US-10-509-422-2	Sequence 2, Appl1
444	48	100.0	570	6	US-10-949-720-386	Sequence 386, App	517	48	100.0	1178	7	US-11-087-099-10105	Sequence 10105, A
445	48	100.0	570	6	US-10-949-720-412	Sequence 412, App	518	48	100.0	1200	7	US-11-207-078-612	Sequence 612, App
446	48	100.0	586	6	US-11-222-451-8	Sequence 8, Appl1	519	48	100.0	1312	7	US-11-067-260-40	Sequence 20, Appl
447	48	100.0	586	6	US-10-623-155-427	Sequence 427, App	520	48	100.0	1312	7	US-11-067-260-32	Sequence 32, Appl
448	48	100.0	589	6	US-10-623-155-486	Sequence 486, App	521	48	100.0	1389	7	US-11-067-260-54	Sequence 52, Appl
449	48	100.0	590	7	US-11-067-260-50	Sequence 50, Appl	522	48	100.0	1392	7	US-11-067-260-22	Sequence 24, Appl
450	48	100.0	593	7	US-11-067-260-20	Sequence 20, Appl	523	48	100.0	1444	7	US-11-067-260-46	Sequence 46, Appl
451	48	100.0	596	7	US-11-201-519-26	Sequence 26, Appl	524	48	100.0	1447	7	US-11-067-260-18	Sequence 18, Appl
452	48	100.0	599	7	US-11-165-141-33	Sequence 33, Appl	525	48	100.0	1474	7	US-11-067-260-18	Sequence 18, Appl
453	48	100.0	600	7	US-11-201-519-22	Sequence 22, Appl	526	48	100.0	1620	6	US-10-453-372-868	Sequence 868, App
454	48	100.0	605	7	US-11-087-099-9709	Sequence 9709, Ap	527	48	100.0	1633	6	US-10-453-372-866	Sequence 866, App
455	48	100.0	608	7	US-11-085-864-2	Sequence 2, Appl1	528	48	100.0	2236	7	US-11-126-113-33	Sequence 33, Appl
456	48	100.0	608	7	US-11-127-004-2	Sequence 2, Appl1	529	48	100.0	2505	7	US-11-126-113-33	Sequence 33, Appl
457	48	100.0	611	7	US-11-130-408-2	Sequence 2, Appl1	530	48	100.0	3353	7	US-11-037-243-64	Sequence 64, Appl
458	48	100.0	611	7	US-11-010-239-129	Sequence 129, App	531	48	100.0	89	9	US-11-096-568A-2163	Sequence 2163, Ap
459	48	100.0	611	7	US-11-087-099-8358	Sequence 8358, App	532	48	100.0	236	7	US-11-096-568A-2162	Sequence 2162, Ap
460	48	100.0	612	7	US-11-087-099-3012	Sequence 3012, Ap	533	48	100.0	309	6	US-11-091-100-15	Sequence 15, Appl
461	48	100.0	612	7	US-11-087-099-6389	Sequence 6389, Ap	534	48	100.0	334	7	US-10-714-887-67	Sequence 67, Appl
462	48	100.0	612	7	US-11-087-099-6541	Sequence 6541, Ap	535	48	100.0	417	7	US-11-096-568A-6229	Sequence 6230, Ap
463	48	100.0	612	7	US-11-087-099-10495	Sequence 10495, A	536	48	100.0	435	7	US-11-096-568A-6228	Sequence 6228, Ap
464	48	100.0	612	7	US-11-067-260-56	Sequence 56, Appl	537	48	100.0	435	7	US-11-096-568A-6228	Sequence 6228, Ap

537	42	87.5	1480	7	US-11-076-074-10	Sequence 10, App1	610	40	83.3	316	7	US-11-096-568A-911	Sequence 911, App
538	42	87.5	1482	7	US-11-181-330-2	Sequence 2, App1	611	40	83.3	317	7	US-11-096-568A-5036	Sequence 5036, App
539	42	87.5	1484	6	US-10-912-971-6	Sequence 6, App1	612	40	83.3	317	7	US-11-096-568A-15449	Sequence 19449, A
540	42	87.5	1484	7	US-11-181-330-6	Sequence 6, App1	613	40	83.3	318	6	US-10-131-826A-374	Sequence 374, App
541	42	87.5	1839	7	US-11-087-099-9631	Sequence 9631, Ap	614	40	83.3	318	6	US-10-973-115B-374	Sequence 19448, A
542	41	85.4	139	6	US-10-793-626-2970	Sequence 2970, Ap	615	40	83.3	320	7	US-11-096-568A-19448	Sequence 19448, A
543	41	85.4	167	7	US-11-096-568A-33470	Sequence 33469, A	616	40	83.3	322	7	US-11-096-568A-12622	Sequence 23622, A
544	41	85.4	198	7	US-11-096-568A-33469	Sequence 33469, A	617	40	83.3	322	7	US-11-096-568A-15863	Sequence 15863, A
545	41	85.4	222	7	US-11-087-099-9791	Sequence 9791, Ap	618	40	83.3	325	7	US-11-096-568A-23621	Sequence 23621, A
546	41	85.4	226	7	US-11-087-099-9791	Sequence 9791, Ap	619	40	83.3	325	7	US-11-096-568A-15862	Sequence 15862, A
547	41	85.4	263	7	US-11-096-568A-10949	Sequence 10949, A	620	40	83.3	326	7	US-11-096-568A-28259	Sequence 28259, A
548	41	85.4	271	7	US-11-096-568A-31149	Sequence 31149, A	621	40	83.3	328	7	US-11-087-099-5132	Sequence 5192, Ap
549	41	85.4	284	6	US-10-714-887-102	Sequence 102, App	622	40	83.3	328	7	US-11-096-568A-23320	Sequence 22320, A
550	41	85.4	286	7	US-11-087-099-420	Sequence 420, App	623	40	83.3	330	6	US-10-714-887-116	Sequence 116, App
551	41	85.4	286	7	US-11-087-099-420	Sequence 420, App	624	40	83.3	330	6	US-11-096-568A-33374	Sequence 33374, A
552	41	85.4	314	7	US-11-096-568A-31147	Sequence 31147, A	625	40	83.3	331	7	US-11-087-099-2717	Sequence 2717, Ap
553	41	85.4	314	7	US-11-096-568A-31147	Sequence 31147, A	626	40	83.3	331	7	US-11-087-099-7366	Sequence 7366, Ap
554	41	85.4	338	7	US-11-087-099-346	Sequence 346, App	627	40	83.3	331	7	US-11-087-099-10734	Sequence 10734, A
555	41	85.4	371	6	US-10-467-962B-41	Sequence 41, App1	628	40	83.3	331	7	US-11-096-568A-19447	Sequence 19447, A
556	41	85.4	384	7	US-11-096-568A-33509	Sequence 33509, A	629	40	83.3	333	7	US-11-096-568A-910	Sequence 910, App
557	41	85.4	386	7	US-11-087-099-12167	Sequence 12167, A	630	40	83.3	336	7	US-11-096-568A-15861	Sequence 15861, A
558	41	85.4	388	7	US-11-096-568A-33508	Sequence 33508, A	631	40	83.3	342	7	US-11-096-568A-33621	Sequence 33621, A
559	41	85.4	388	7	US-11-096-568A-33508	Sequence 33508, A	632	40	83.3	343	7	US-11-225-709-1	Sequence 1, App1
560	41	85.4	396	7	US-11-096-568A-33507	Sequence 33507, A	633	40	83.3	344	7	US-11-096-568A-33373	Sequence 33373, A
561	41	85.4	409	7	US-11-096-568A-10947	Sequence 10947, A	634	40	83.3	347	7	US-11-096-568A-20943	Sequence 20943, A
562	41	85.4	551	7	US-11-096-568A-32057	Sequence 32057, A	635	40	83.3	347	7	US-11-096-568A-25772	Sequence 25772, A
563	41	85.4	577	7	US-11-096-568A-32056	Sequence 32056, A	636	40	83.3	353	7	US-11-096-568A-25771	Sequence 25771, A
564	41	85.4	745	7	US-11-147-109-8	Sequence 8, App1	637	40	83.3	355	7	US-11-096-568A-33620	Sequence 33620, A
565	40	83.3	1516	6	US-10-501-035-284	Sequence 284, App	638	40	83.3	357	7	US-11-087-099-5803	Sequence 5803, Ap
566	40	83.3	5	6	US-10-989-226-9	Sequence 9, App1	639	40	83.3	360	7	US-11-096-568A-15133	Sequence 15133, A
567	40	83.3	5	7	US-11-006-031-19	Sequence 19, App1	640	40	83.3	360	7	US-11-096-568A-15133	Sequence 15133, A
568	40	83.3	5	7	US-11-066-967-36	Sequence 36, App1	641	40	83.3	361	7	US-11-096-568A-23620	Sequence 23620, A
569	40	83.3	5	7	US-11-194-110-19	Sequence 19, App1	642	40	83.3	362	7	US-11-096-568A-4672	Sequence 4672, Ap
570	40	83.3	6	7	US-11-189-321-51	Sequence 11, App1	643	40	83.3	368	7	US-11-096-568A-15485	Sequence 15485, A
571	40	83.3	12	6	US-10-507-028-3	Sequence 3, App1	644	40	83.3	377	7	US-11-087-099-11030	Sequence 11030, A
572	40	83.3	64	6	US-10-952-535A-23	Sequence 23, App1	645	40	83.3	378	7	US-11-096-568A-4671	Sequence 4671, Ap
573	40	83.3	69	6	US-10-952-535A-9	Sequence 9, App1	646	40	83.3	381	7	US-11-185-859-6	Sequence 6, App1
574	40	83.3	113	6	US-10-952-535A-20	Sequence 20, App1	647	40	83.3	382	7	US-11-054-428-1104	Sequence 104, App1
575	40	83.3	115	7	US-11-072-512-2510	Sequence 210, App	648	40	83.3	386	7	US-11-096-568A-4670	Sequence 4670, Ap
576	40	83.3	150	7	US-11-087-099-4618	Sequence 4618, Ap	649	40	83.3	388	7	US-11-087-099-8387	Sequence 8387, Ap
577	40	83.3	184	7	US-11-087-099-6552	Sequence 6552, Ap	650	40	83.3	394	7	US-11-055-822-1094	Sequence 1094, Ap
578	40	83.3	192	6	US-10-990-627-12	Sequence 12, App1	651	40	83.3	398	7	US-11-096-568A-33372	Sequence 33372, A
579	40	83.3	195	7	US-11-096-568A-21315	Sequence 21315, A	652	40	83.3	399	7	US-11-096-568A-15132	Sequence 15132, A
580	40	83.3	213	6	US-10-990-627-1	Sequence 1, App1	653	40	83.3	411	7	US-11-096-568A-18058	Sequence 18058, A
581	40	83.3	218	7	US-11-096-568A-24967	Sequence 24967, A	654	40	83.3	411	7	US-11-096-568A-27631	Sequence 27631, A
582	40	83.3	223	7	US-11-096-568A-15487	Sequence 15487, A	655	40	83.3	414	7	US-11-096-568A-15131	Sequence 15131, A
583	40	83.3	224	6	US-10-714-887-340	Sequence 340, App	656	40	83.3	417	6	US-10-971-560-4	Sequence 4, App1
584	40	83.3	234	6	US-11-096-568A-20994	Sequence 20994, A	657	40	83.3	424	7	US-11-096-568A-24510	Sequence 24510, A
585	40	83.3	240	6	US-10-467-657-9060	Sequence 9060, App	658	40	83.3	430	7	US-11-096-568A-27630	Sequence 27630, A
586	40	83.3	243	7	US-11-096-568A-24644	Sequence 24644, A	659	40	83.3	430	7	US-11-096-568A-29710	Sequence 29710, A
587	40	83.3	244	7	US-11-087-099-9043	Sequence 9043, Ap	660	40	83.3	437	6	US-10-453-372-438	Sequence 438, App
588	40	83.3	247	7	US-11-096-568A-21961	Sequence 21961, A	661	40	83.3	438	7	US-11-096-568A-25770	Sequence 25770, A
589	40	83.3	254	7	US-11-004-399-620	Sequence 620, App	662	40	83.3	441	7	US-11-096-568A-15595	Sequence 15595, A
590	40	83.3	257	7	US-11-096-568A-20993	Sequence 20993, A	663	40	83.3	446	7	US-11-096-568A-25708	Sequence 25708, A
591	40	83.3	257	7	US-11-096-568A-24966	Sequence 24966, A	664	40	83.3	468	7	US-10-878-556A-101	Sequence 101, App
592	40	83.3	264	6	US-10-714-887-108	Sequence 108, App	665	40	83.3	470	6	US-11-087-099-12191	Sequence 12191, A
593	40	83.3	266	7	US-11-096-568A-20944	Sequence 20944, A	666	40	83.3	480	7	US-11-132-142-6	Sequence 6, App1
594	40	83.3	269	7	US-11-096-568A-9091	Sequence 9091, App	667	40	83.3	493	7	US-11-010-239-81	Sequence 81, App1
595	40	83.3	271	7	US-11-096-568A-9093	Sequence 9093, App	668	40	83.3	494	6	US-10-971-560-2	Sequence 4, App1
596	40	83.3	271	7	US-11-096-568A-1301	Sequence 1301, App	669	40	83.3	501	6	US-10-971-560-7	Sequence 2, App1
597	40	83.3	275	7	US-11-096-568A-15046	Sequence 15046, A	670	40	83.3	504	6	US-10-971-560-2	Sequence 10, App1
598	40	83.3	276	7	US-11-091-100-16	Sequence 16, App1	671	40	83.3	501	6	US-10-971-560-10	Sequence 10, App1
599	40	83.3	276	7	US-11-096-568A-15486	Sequence 15486, A	672	40	83.3	501	6	US-10-500-441-1	Sequence 1, App1
600	40	83.3	277	6	US-10-793-626-314	Sequence 314, App	673	40	83.3	501	7	US-11-067-121-1	Sequence 1, App1
601	40	83.3	277	6	US-10-793-626-314	Sequence 314, App	674	40	83.3	501	7	US-11-076-427A-2	Sequence 2, App1
602	40	83.3	279	7	US-11-096-568A-1300	Sequence 1300, App	675	40	83.3	513	6	US-10-453-372-442	Sequence 442, App
603	40	83.3	285	7	US-11-096-568A-1299	Sequence 1299, App	676	40	83.3	519	7	US-11-096-568A-33698	Sequence 33698, A
604	40	83.3	287	7	US-11-096-568A-5037	Sequence 5037, App	677	40	83.3	519	7	US-11-096-568A-24530	Sequence 24530, A
605	40	83.3	290	7	US-11-096-568A-18388	Sequence 18388, A	678	40	83.3	523	7	US-11-096-568A-24529	Sequence 24529, A
606	40	83.3	291	7	US-11-087-099-9426	Sequence 9426, App	679	40	83.3	527	7	US-11-087-099-1291	Sequence 1291, Ap
607	40	83.3	291	7	US-11-087-099-9235	Sequence 9235, App	680	40	83.3	532	7	US-11-087-099-340	Sequence 340, App
608	40	83.3	299	7	US-11-096-568A-22321	Sequence 22321, A	681	40	83.3	535	6	US-10-453-372-436	Sequence 436, App
609	40	83.3	300	7	US-11-096-568A-27632	Sequence 27632, A	682	40	83.3	541	7	US-11-096-568A-20889	Sequence 20889, A

683	40	83.3	541	7	US-11-096-568A-33697	Sequence 33697, A	756	37	77.1	436	7	US-11-042-814-4	Sequence 4, Appl1
684	40	83.3	593	7	US-11-087-099-3921	Sequence 3921, Ap	757	37	77.1	498	7	US-11-096-568A-157	Sequence 157, App
685	40	83.3	593	7	US-11-087-099-5800	Sequence 5800, Ap	758	37	77.1	564	7	US-11-087-099-9918	Sequence 9918, Ap
686	40	83.3	635	7	US-11-096-568A-22628	Sequence 22628, A	759	37	77.1	578	7	US-11-096-568A-156	Sequence 156, App
687	40	83.3	635	7	US-11-096-568A-27797	Sequence 27797, A	760	37	77.1	534	7	US-11-096-568A-155	Sequence 155, App
688	40	83.3	646	7	US-11-004-399-289	Sequence 289, App	761	37	77.1	710	7	US-11-096-568A-158	Sequence 158, App
689	40	83.3	676	7	US-11-004-399-3931	Sequence 3931, Ap	762	37	77.1	900	6	US-10-501-033-215	Sequence 215, App
690	40	83.3	699	7	US-11-138-642-4	Sequence 4, Appl1	763	36.5	76.0	331	7	US-11-087-099-457	Sequence 457, App
691	40	83.3	699	7	US-11-138-882-5	Sequence 5, Appl1	764	36.5	76.0	449	7	US-11-096-568A-19441	Sequence 19441, A
692	40	83.3	699	7	US-11-138-757-5	Sequence 5, Appl1	765	36.5	76.0	455	7	US-11-096-568A-19439	Sequence 19439, A
693	40	83.3	710	7	US-11-096-568A-22627	Sequence 22627, A	766	36.5	76.0	457	7	US-11-096-568A-19439	Sequence 19439, A
694	40	83.3	737	6	US-10-453-372-434	Sequence 434, App	767	36.5	76.0	828	7	US-11-096-568A-27590	Sequence 27590, A
695	40	83.3	737	6	US-10-453-372-446	Sequence 446, App	768	36.5	76.0	846	7	US-11-096-568A-27850	Sequence 27850, A
696	40	83.3	737	6	US-10-453-372-448	Sequence 448, App	769	36	75.0	173	7	US-11-096-568A-29045	Sequence 29046, A
697	40	83.3	737	6	US-10-453-372-450	Sequence 450, App	770	36	75.0	231	7	US-11-096-568A-23503	Sequence 23503, A
698	40	83.3	737	6	US-10-453-372-452	Sequence 452, App	771	36	75.0	319	6	US-10-714-887-104	Sequence 104, App
699	40	83.3	737	6	US-10-453-372-454	Sequence 454, App	772	36	75.0	237	6	US-10-793-652-2368	Sequence 2368, Ap
700	40	83.3	737	6	US-10-453-372-456	Sequence 456, App	773	36	75.0	368	7	US-11-096-568A-22501	Sequence 22501, A
701	40	83.3	749	7	US-11-054-281-103	Sequence 103, App	774	36	75.0	380	7	US-11-096-568A-27808	Sequence 27808, A
702	40	83.3	752	7	US-11-080-991-52	Sequence 52, Appl	775	35.5	74.0	576	7	US-11-087-099-3700	Sequence 3700, Ap
703	40	83.3	752	7	US-11-054-281-101	Sequence 101, App	776	35.5	74.0	577	7	US-11-087-099-3883	Sequence 3883, Ap
704	40	83.3	755	6	US-10-453-372-1108	Sequence 1108, Ap	777	35.5	74.0	577	7	US-11-087-099-3883	Sequence 3883, Ap
705	40	83.3	755	6	US-11-054-281-26	Sequence 26, Appl	778	35	72.9	268	7	US-11-087-099-11276	Sequence 11276, A
706	40	83.3	755	7	US-11-054-281-102	Sequence 102, App	779	35	72.9	914	6	US-10-312-954-2	Sequence 2, Appl1
707	40	83.3	884	7	US-11-087-099-11219	Sequence 11219, A	780	34	70.8	9	6	US-10-895-064-1823	Sequence 1823, Ap
708	40	83.3	1035	7	US-11-087-099-5013	Sequence 5013, Ap	781	34	70.8	12	7	US-11-129-741-1823	Sequence 1823, Ap
709	40	83.3	1607	7	US-11-098-686-10178	Sequence 10178, A	782	34	70.8	9	7	US-11-145-035-32	Sequence 32, Appl
710	40	83.3	2333	7	US-11-096-281-13	Sequence 13, Appl	783	34	70.8	70	6	US-10-467-657-8668	Sequence 8668, Ap
711	40	83.3	2339	7	US-11-096-281-11	Sequence 11, Appl	784	34	70.8	84	7	US-11-138-642-9	Sequence 9, Appl1
712	39	81.2	227	7	US-11-096-568A-26075	Sequence 26075, A	785	34	70.8	84	7	US-11-138-882-9	Sequence 9, Appl1
713	39	81.2	310	6	US-10-714-887-52	Sequence 52, Appl	786	34	70.8	84	7	US-11-138-757-10	Sequence 10, Appl
714	39	81.2	312	6	US-10-714-887-54	Sequence 54, Appl	787	34	70.8	151	6	US-10-467-657-1332	Sequence 132, App
715	39	81.2	329	6	US-10-467-657-2240	Sequence 2240, App	788	34	70.8	151	6	US-10-467-657-5856	Sequence 5856, Ap
716	39	81.2	344	7	US-11-087-099-37305	Sequence 37305, Ap	789	34	70.8	181	7	US-11-098-686-10422	Sequence 10422, A
717	39	81.2	350	7	US-11-087-099-955	Sequence 955, App	790	34	70.8	193	7	US-11-087-099-9209	Sequence 9209, Ap
718	39	81.2	457	7	US-11-169-041-212	Sequence 212, App	791	34	70.8	222	7	US-11-096-568A-8937	Sequence 8937, Ap
719	39	81.2	730	6	US-10-453-372-444	Sequence 444, App	792	34	70.8	235	7	US-11-096-568A-83343	Sequence 83343, A
720	38	79.2	12	6	US-10-507-028-7	Sequence 7, Appl1	793	34	70.8	242	6	US-10-524-647-6	Sequence 6, Appl1
721	38	79.2	95	7	US-11-096-568A-4472	Sequence 4472, Ap	794	34	70.8	242	6	US-10-524-647-8	Sequence 8, Appl1
722	38	79.2	97	7	US-11-096-568A-4471	Sequence 4471, Ap	795	34	70.8	242	6	US-10-524-647-10	Sequence 10, Appl
723	38	79.2	218	7	US-11-096-568A-7822	Sequence 7822, Ap	796	34	70.8	242	6	US-10-524-647-100	Sequence 100, App
724	38	79.2	275	7	US-11-096-568A-22436	Sequence 22436, A	797	34	70.8	242	6	US-10-524-972-6	Sequence 6, Appl1
725	38	79.2	304	7	US-11-096-568A-7821	Sequence 7821, Ap	798	34	70.8	242	6	US-10-524-972-8	Sequence 8, Appl1
726	38	79.2	311	7	US-11-108-172-1061	Sequence 1061, Ap	799	34	70.8	242	6	US-10-524-972-10	Sequence 10, Appl
727	38	79.2	339	7	US-11-096-568A-1738	Sequence 1738, Ap	800	34	70.8	242	6	US-11-129-143-181	Sequence 181, App
728	38	79.2	347	7	US-11-096-568A-1737	Sequence 1737, Ap	801	34	70.8	242	7	US-11-070-080-33	Sequence 33, Appl
729	38	79.2	353	7	US-11-096-568A-24793	Sequence 24793, A	802	34	70.8	242	7	US-11-087-099-328	Sequence 328, App
730	38	79.2	364	7	US-11-096-568A-7820	Sequence 7820, Ap	803	34	70.8	257	7	US-10-714-887-248	Sequence 248, App
731	38	79.2	376	7	US-11-096-568A-22435	Sequence 22435, A	804	34	70.8	265	6	US-10-714-887-106	Sequence 106, App
732	38	79.2	376	7	US-11-087-099-6961	Sequence 6961, Ap	805	34	70.8	315	6	US-10-714-887-282	Sequence 282, App
733	38	79.2	376	7	US-11-087-099-12395	Sequence 12395, A	806	34	70.8	320	7	US-11-132-864-31	Sequence 31, Appl
734	38	79.2	380	7	US-11-087-099-1772	Sequence 1772, Ap	807	34	70.8	325	7	US-11-096-568A-23538	Sequence 23538, A
735	38	79.2	380	7	US-11-087-099-9164	Sequence 9164, Ap	808	34	70.8	325	7	US-11-096-568A-23537	Sequence 23537, A
736	38	79.2	380	7	US-11-087-099-9819	Sequence 9819, Ap	809	34	70.8	325	7	US-11-096-568A-23537	Sequence 23537, A
737	38	79.2	381	7	US-11-146-428-73	Sequence 73, Appl	810	34	70.8	387	7	US-11-096-568A-33342	Sequence 33342, A
738	38	79.2	381	7	US-11-096-568A-22434	Sequence 22434, A	811	34	70.8	402	7	US-11-183-664-94	Sequence 94, Appl
739	38	79.2	393	7	US-11-096-568A-23670	Sequence 23670, A	812	34	70.8	402	7	US-11-087-099-9341	Sequence 9341, Ap
740	38	79.2	419	7	US-11-096-568A-1102	Sequence 1102, Ap	813	34	70.8	449	7	US-11-018-868-49	Sequence 49, Appl
741	38	79.2	435	7	US-11-096-568A-1101	Sequence 1101, Ap	814	34	70.8	453	7	US-11-096-568A-27953	Sequence 27953, A
742	38	79.2	446	7	US-11-096-568A-1100	Sequence 1100, Ap	815	34	70.8	472	7	US-11-087-099-10553	Sequence 10553, A
743	38	79.2	470	7	US-11-096-568A-23669	Sequence 23669, A	816	34	70.8	531	7	US-11-010-239-32	Sequence 32, Appl
744	38	79.2	504	7	US-11-096-568A-23668	Sequence 23668, A	817	34	70.8	608	7	US-11-087-099-8952	Sequence 8952, Ap
745	38	79.2	643	7	US-11-120-544B-2	Sequence 2, Appl1	818	34	70.8	608	7	US-11-087-099-9341	Sequence 9341, Ap
746	38	79.2	1138	6	US-10-509-422-4	Sequence 4, Appl1	819	34	70.8	783	7	US-11-186-284-59	Sequence 59, Appl
747	37.5	78.1	570	7	US-11-087-099-304	Sequence 304, App	820	34	70.8	2151	7	US-11-126-313-31	Sequence 31, Appl
748	37.5	78.1	570	7	US-11-072-512-2718	Sequence 2718, App	821	34	68.8	123	6	US-10-467-657-2322	Sequence 2322, App
749	37.5	78.1	823	7	US-11-166-892-4	Sequence 4, Appl1	822	33	68.8	165	6	US-11-096-568A-28780	Sequence 28780, A
750	37	77.1	12	6	US-10-507-028-6	Sequence 6, Appl1	823	33	68.8	219	7	US-11-096-568A-33207	Sequence 32107, A
751	37	77.1	180	7	US-11-096-568A-10886	Sequence 10886, A	824	33	68.8	224	7	US-11-096-568A-332106	Sequence 32106, A
752	37	77.1	185	7	US-11-096-568A-10885	Sequence 10885, A	825	33	68.8	228	7	US-11-087-099-7368	Sequence 7368, Ap
753	37	77.1	249	7	US-11-096-568A-10884	Sequence 10884, A	826	33	68.8	228	7	US-11-087-099-7368	Sequence 7368, Ap
754	37	77.1	260	7	US-11-096-568A-11763	Sequence 11763, A	827	33	68.8	225	7	US-11-096-568A-32032	Sequence 32032, A
755	37	77.1	422	7	US-11-096-568A-7023	Sequence 7023, Ap	828	33	68.8	258	7	US-11-096-568A-32031	Sequence 32031, A

829	33	68.8	266	7	US-11-072-512-3891	Sequence 3891, Ap	902	32	66.7	203	7	US-11-087-099-8087	Sequence 8087, Ap
830	33	68.8	267	7	US-11-096-568A-26429	Sequence 26429, A	903	32	66.7	203	7	US-11-096-568A-9313	Sequence 9313, Ap
831	33	68.8	268	7	US-11-096-568A-5163	Sequence 5163, Ap	904	32	66.7	203	7	US-11-096-568A-9315	Sequence 9315, Ap
832	33	68.8	269	7	US-11-096-568A-1487	Sequence 1487, Ap	905	32	66.7	212	7	US-11-096-568A-12896	Sequence 12896, A
833	33	68.8	281	6	US-10-714-887-240	Sequence 240, App	906	32	66.7	212	7	US-11-096-568A-782	Sequence 782, App
834	33	68.8	286	7	US-11-096-568A-26428	Sequence 26428, A	907	32	66.7	221	7	US-11-096-568A-26474	Sequence 26474, A
835	33	68.8	296	6	US-11-096-568A-25814	Sequence 25814, A	908	32	66.7	223	7	US-11-096-568A-14586	Sequence 14586, A
836	33	68.8	300	6	US-10-667-295-117	Sequence 117, App	909	32	66.7	234	7	US-11-096-568A-9312	Sequence 9312, Ap
837	33	68.8	302	6	US-10-667-295-116	Sequence 116, App	910	32	66.7	235	7	US-11-096-568A-21210	Sequence 21210, A
838	33	68.8	307	7	US-11-096-568A-5162	Sequence 5162, Ap	911	32	66.7	237	7	US-11-096-568A-112	Sequence 112, App
839	33	68.8	316	6	US-10-667-295-115	Sequence 115, App	912	32	66.7	240	7	US-11-096-568A-4645	Sequence 4645, Ap
840	33	68.8	318	7	US-11-096-568A-5161	Sequence 5161, Ap	913	32	66.7	243	7	US-11-096-568A-12443	Sequence 12443, A
841	33	68.8	325	7	US-11-096-568A-32030	Sequence 32030, A	914	32	66.7	244	6	US-10-524-647-102	Sequence 1045, A
842	33	68.8	335	7	US-11-096-568A-18414	Sequence 18414, A	915	32	66.7	246	6	US-10-524-972-86	Sequence 86, App1
843	33	68.8	336	7	US-11-096-568A-15920	Sequence 15920, A	916	32	66.7	250	7	US-11-096-568A-19825	Sequence 19825, A
844	33	68.8	337	7	US-11-096-568A-18413	Sequence 18413, A	917	32	66.7	255	7	US-11-087-099-1551	Sequence 1551, Ap
845	33	68.8	356	7	US-11-096-568A-29211	Sequence 29211, A	918	32	66.7	258	6	US-10-524-647-14	Sequence 14, App1
846	33	68.8	360	7	US-11-096-568A-29210	Sequence 29210, A	919	32	66.7	258	6	US-10-524-972-114	Sequence 14, App1
847	33	68.8	369	7	US-11-096-568A-29209	Sequence 29209, A	920	32	66.7	264	7	US-11-096-568A-11433	Sequence 11433, A
848	33	68.8	378	7	US-11-096-568A-18412	Sequence 18412, A	921	32	66.7	267	7	US-11-096-568A-20465	Sequence 20465, A
849	33	68.8	383	6	US-10-537-897-42	Sequence 42, App1	922	32	66.7	271	6	US-10-714-887-48	Sequence 48, App1
850	33	68.8	385	7	US-11-096-568A-4426	Sequence 4426, Ap	923	32	66.7	271	7	US-11-096-568A-30118	Sequence 30118, A
851	33	68.8	395	7	US-11-096-568A-4425	Sequence 4425, Ap	924	32	66.7	273	7	US-11-087-099-11050	Sequence 11050, A
852	33	68.8	398	6	US-10-991-285-894	Sequence 894, App	925	32	66.7	273	7	US-11-087-099-12279	Sequence 12279, A
853	33	68.8	398	7	US-11-087-099-5162	Sequence 5162, App	926	32	66.7	273	7	US-11-096-568A-27047	Sequence 27047, A
854	33	68.8	448	6	US-10-312-954-4	Sequence 4, App1	927	32	66.7	280	7	US-11-096-568A-6891	Sequence 6891, Ap
855	33	68.8	449	6	US-11-096-568A-15309	Sequence 15309, A	928	32	66.7	280	7	US-11-096-568A-15872	Sequence 15872, A
856	33	68.8	451	6	US-10-714-887-182	Sequence 182, App	929	32	66.7	282	7	US-11-096-568A-21209	Sequence 21209, A
857	33	68.8	459	6	US-10-467-657-8726	Sequence 8726, Ap	930	32	66.7	288	7	US-11-096-568A-10047	Sequence 10047, A
858	33	68.8	471	7	US-11-087-099-5840	Sequence 5840, Ap	931	32	66.7	288	7	US-11-096-568A-12950	Sequence 12950, A
859	33	68.8	533	6	US-10-467-657-9063	Sequence 9063, Ap	932	32	66.7	288	7	US-11-096-568A-22903	Sequence 22903, A
860	33	68.8	611	7	US-11-087-099-6674	Sequence 6674, Ap	933	32	66.7	291	7	US-11-096-568A-6690	Sequence 6690, Ap
861	33	68.8	684	7	US-11-096-568A-9418	Sequence 9418, Ap	934	32	66.7	292	7	US-11-096-568A-26427	Sequence 26427, A
862	33	68.8	711	7	US-11-096-568A-9417	Sequence 9417, Ap	935	32	66.7	297	7	US-11-096-568A-17628	Sequence 17628, A
863	33	68.8	2145	7	US-11-087-099-10331	Sequence 10331, A	936	32	66.7	294	7	US-11-096-568A-21208	Sequence 21208, A
864	32.5	67.7	283	7	US-11-096-568A-13650	Sequence 13650, A	937	32	66.7	296	6	US-10-714-887-226	Sequence 226, App
865	32.5	67.7	337	7	US-11-096-568A-13649	Sequence 13649, A	938	32	66.7	296	7	US-11-096-568A-21195	Sequence 21195, A
866	32.5	67.7	791	7	US-11-096-568A-17894	Sequence 17894, A	939	32	66.7	297	7	US-11-096-568A-24051	Sequence 24051, A
867	32.5	67.7	877	7	US-11-087-099-9802	Sequence 9802, Ap	940	32	66.7	297	7	US-11-087-099-9568	Sequence 9568, A
868	32.5	67.7	877	7	US-11-087-099-12075	Sequence 12075, A	941	32	66.7	300	7	US-11-096-568A-24050	Sequence 24050, A
869	32	66.7	8	7	US-11-145-035-34	Sequence 34, App1	942	32	66.7	308	7	US-11-052-5544-251	Sequence 251, App
870	32	66.7	10	6	US-10-498-665-74	Sequence 74, App1	943	32	66.7	308	7	US-11-096-568A-22902	Sequence 22902, A
871	32	66.7	10	6	US-10-498-665-74	Sequence 74, App1	944	32	66.7	309	7	US-11-087-099-2169	Sequence 2169, Ap
872	32	66.7	10	7	US-11-158-848-37	Sequence 37, App1	945	32	66.7	309	7	US-11-087-099-7821	Sequence 7821, Ap
873	32	66.7	13	7	US-11-004-399-3100	Sequence 3100, Ap	946	32	66.7	310	7	US-11-072-512-3795	Sequence 3795, Ap
874	32	66.7	14	7	US-11-051-120-1771	Sequence 1771, Ap	947	32	66.7	310	7	US-11-087-099-11476	Sequence 11476, A
875	32	66.7	14	7	US-11-043-806-542	Sequence 542, App	948	32	66.7	311	6	US-10-714-887-298	Sequence 298, App
876	32	66.7	17	6	US-10-895-064-2213	Sequence 2213, Ap	949	32	66.7	311	7	US-11-096-568A-1962	Sequence 1962, Ap
877	32	66.7	17	7	US-11-129-741-2213	Sequence 2213, Ap	950	32	66.7	311	7	US-11-096-568A-6889	Sequence 6889, Ap
878	32	66.7	17	7	US-11-152-974A-151	Sequence 151, App	951	32	66.7	313	7	US-11-096-568A-24049	Sequence 24049, A
879	32	66.7	17	7	US-11-153-143A-151	Sequence 151, App	952	32	66.7	313	7	US-11-096-568A-9927	Sequence 9927, Ap
880	32	66.7	29	7	US-11-108-185-51	Sequence 51, App1	953	32	66.7	316	7	US-11-096-568A-17627	Sequence 17627, A
881	32	66.7	80	7	US-11-051-720-1312	Sequence 1312, Ap	954	32	66.7	319	7	US-11-087-099-455	Sequence 455, App
882	32	66.7	80	7	US-11-043-806-337	Sequence 337, App	955	32	66.7	319	7	US-11-087-099-4262	Sequence 4262, Ap
883	32	66.7	84	7	US-11-096-568A-6467	Sequence 6467, Ap	956	32	66.7	325	7	US-11-096-568A-11432	Sequence 11432, A
884	32	66.7	97	7	US-11-096-568A-4955	Sequence 4955, Ap	957	32	66.7	325	7	US-11-096-568A-21193	Sequence 21193, A
885	32	66.7	132	7	US-11-096-568A-11864	Sequence 11864, A	958	32	66.7	337	7	US-11-096-568A-22901	Sequence 22901, A
886	32	66.7	132	7	US-11-096-568A-11863	Sequence 11863, A	959	32	66.7	337	7	US-11-096-568A-25427	Sequence 25427, A
887	32	66.7	137	6	US-10-821-234-1242	Sequence 1242, Ap	960	32	66.7	339	7	US-11-096-568A-11851	Sequence 11851, A
888	32	66.7	143	7	US-11-096-568A-11862	Sequence 11862, A	961	32	66.7	344	7	US-11-096-568A-31491	Sequence 31491, A
889	32	66.7	155	7	US-11-096-568A-12951	Sequence 12951, A	962	32	66.7	345	7	US-11-087-099-11205	Sequence 11205, A
890	32	66.7	161	7	US-11-096-568A-9092	Sequence 9092, Ap	963	32	66.7	345	7	US-11-096-568A-3856	Sequence 3856, A
891	32	66.7	164	7	US-11-096-568A-16620	Sequence 16620, A	964	32	66.7	347	7	US-11-087-099-1768	Sequence 1768, Ap
892	32	66.7	167	7	US-11-096-568A-10793	Sequence 10793, A	965	32	66.7	348	7	US-11-096-568A-31490	Sequence 31490, A
893	32	66.7	170	7	US-11-096-568A-19659	Sequence 19659, A	966	32	66.7	350	7	US-11-087-099-3229	Sequence 3229, Ap
894	32	66.7	176	6	US-10-467-657-5812	Sequence 5812, Ap	967	32	66.7	350	7	US-11-087-099-8373	Sequence 8373, Ap
895	32	66.7	182	7	US-11-087-099-7260	Sequence 7260, Ap	968	32	66.7	351	7	US-11-096-568A-33855	Sequence 33855, A
896	32	66.7	187	7	US-11-087-099-9919	Sequence 9919, Ap	969	32	66.7	353	7	US-11-096-568A-15722	Sequence 15722, A
897	32	66.7	187	7	US-11-096-568A-19658	Sequence 19658, A	970	32	66.7	354	7	US-11-072-512-3151	Sequence 3151, Ap
898	32	66.7	189	7	US-11-096-568A-9314	Sequence 9314, Ap	971	32	66.7	356	7	US-11-096-568A-1161	Sequence 1161, Ap
899	32	66.7	195	7	US-11-096-568A-4197	Sequence 4197, Ap	972	32	66.7	356	7	US-11-096-568A-31489	Sequence 31489, A
900	32	66.7	200	7	US-11-096-568A-784	Sequence 784, App	973	32	66.7	357	7	US-11-096-568A-11850	Sequence 11850, A
901	32	66.7	201	7	US-11-096-568A-783	Sequence 783, App	974	32	66.7	358	7	US-11-146-428-112	Sequence 112, App

```
975 32 66.7 361 7 US-11-096-568A-23570 Sequence 23570, A
976 32 66.7 364 7 US-11-096-568A-22226 Sequence 22226, A
977 32 66.7 367 7 US-11-096-568A-19569 Sequence 19569, A
978 32 66.7 368 7 US-11-096-568A-11631 Sequence 11631, A
979 32 66.7 374 7 US-11-096-568A-19568 Sequence 19568, A
980 32 66.7 376 7 US-11-096-568A-18596 Sequence 18596, A
981 32 66.7 376 7 US-11-096-568A-33854 Sequence 33854, A
982 32 66.7 378 7 US-11-087-099-12233 Sequence 12233, A
983 32 66.7 378 7 US-11-096-568A-12553 Sequence 12553, A
984 32 66.7 383 7 US-11-096-568A-16959 Sequence 16959, A
985 32 66.7 387 6 US-10-714-887-176 Sequence 176, App
986 32 66.7 392 7 US-11-087-099-11744 Sequence 11744, A
987 32 66.7 399 7 US-11-096-568A-11431 Sequence 11431, A
988 32 66.7 403 7 US-11-146-428-90 Sequence 90, Appl
989 32 66.7 406 7 US-11-096-568A-11630 Sequence 11630, A
990 32 66.7 409 7 US-11-087-099-6807 Sequence 6807, Ap
991 32 66.7 411 7 US-11-087-099-6317 Sequence 6317, Ap
992 32 66.7 411 7 US-11-087-099-7760 Sequence 7760, Ap
993 32 66.7 413 7 US-11-096-568A-22225 Sequence 22225, A
994 32 66.7 414 7 US-11-115-868-2 Sequence 2, Appl
995 32 66.7 417 7 US-11-165-305-2 Sequence 2, Appl
996 32 66.7 417 7 US-11-096-568A-19567 Sequence 19567, A
997 32 66.7 419 7 US-11-096-568A-10209 Sequence 10209, A
998 32 66.7 420 7 US-11-096-568A-23920 Sequence 23920, A
999 32 66.7 421 7 US-11-096-568A-11629 Sequence 11629, A
1000 32 66.7 424 7 US-11-096-568A-23919 Sequence 23919, A
```

ALIGNMENTS

```
RESULT 1
US-10-512-184-46
; Sequence 46, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: His6 tag
US-10-512-184-46

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 2
US-10-967-671-18
; Sequence 18, Application US/10967671
; Publication No. US20050245728A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; APPLICANT: KIMBER, MATTHEW
; APPLICANT: VALLEE, FRANCOIS
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM PSEUDOMONAS AERUGINOSA
```

```
; FILE REFERENCE: IPT-261.01
; CURRENT APPLICATION NUMBER: US/10/967,671
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: PCT/CA03/00714
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 60/382,443
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-967-671-18

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 3
US-10-966-648-29
; Sequence 29, Application US/10966648
; Publication No. US20050249734A1
; GENERAL INFORMATION:
; APPLICANT: Sutcliffe, J. Gregor
; APPLICANT: de Leca, Luis
; APPLICANT: Henriksen, Steven J.
; APPLICANT: Stiggins, George R.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
; FILE REFERENCE: 14740A-000640US
; CURRENT APPLICATION NUMBER: US/10/966,648
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US 08/648,322
; PRIOR FILING DATE: 1996-05-15
; PRIOR APPLICATION NUMBER: US 08/857,389
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: US 09/766,396
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6xHis tag
US-10-966-648-29

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 4
US-10-497-767-5
; Sequence 5, Application US/10497767
; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
```

```
APPLICANT: SWENSON, LOVORKA
TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
TITLE OF INVENTION: THERBOP
FILE REFERENCE: VPI/01-13 PCT
CURRENT APPLICATION NUMBER: US/10/497,767
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 60/337,513
PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6x-His tag
US-10-497-767-5

Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6

RESULT 5
US-10-983-174-1
Sequence 1, Application US/10983174
Publication No. US20050261307A1
GENERAL INFORMATION:
APPLICANT: CAI, SHAOPEI
APPLICANT: CHOU, Joice
APPLICANT: HARWOOD, ERIC
APPLICANT: HEISE, CARLA C.
APPLICANT: MACHAJEWSKI, TIMOTHY D.
APPLICANT: RYCKMAN, DAVID
APPLICANT: SHANG, XIAO
APPLICANT: WIESMANN, MARION
APPLICANT: ZHU, SHUGUANG
TITLE OF INVENTION: INHIBITION OF FGFR3 AND TREATMENT OF MULTIPLE MYELOMA
FILE REFERENCE: 072121-0445
CURRENT APPLICATION NUMBER: US/10/983,174
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: 60/546,017
PRIOR FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: 60/526,425
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/526,426
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/517,915
PRIOR FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: 10/644,055
PRIOR FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: 60/405,729
PRIOR FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: 60/428,210
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: 60/484,048
PRIOR FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: 60/426,282
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 60/460,493
PRIOR FILING DATE: 2003-04-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 1
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
```

```
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-983-174-1

Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6

RESULT 6
US-10-475-204-28
Sequence 28, Application US/10475204
Publication No. US20050277116A1
GENERAL INFORMATION:
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION OF
TITLE OF INVENTION: PROTEIN INTERACTIONS IN VERTEBRATE CELLS
FILE REFERENCE: HMY-056.25
CURRENT APPLICATION NUMBER: US/10/475,204
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/US02/13008
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: 60/285,509
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6x
US-10-475-204-28

Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6

RESULT 7
US-10-957-351-357
Sequence 357, Application US/10957351
Publication No. US20060008844A1
GENERAL INFORMATION:
APPLICANT: Stemmer, Willem P. C.
APPLICANT: Perltroth, D. Victor
APPLICANT: Satval, Sanjeev
APPLICANT: Avidia Research Institute
TITLE OF INVENTION: C-Met Kinase Binding Proteins
FILE REFERENCE: 022013-001400US
CURRENT APPLICATION NUMBER: US/10/957,351
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 10/871,602
PRIOR FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 471
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 357
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 6xHis, hexahistidine tag
US-10-957-351-357
```

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 8
US-10-895-064-27
; Sequence 27, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; APPLICANT: LEUNG, FREDERICK C.
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
; FILE REFERENCE: V0690.0031
; CURRENT APPLICATION NUMBER: US/10/895,064
; CURRENT FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 2918
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: -His tag
US-10-895-064-27

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 9
US-10-950-747-12
; Sequence 12, Application US/10950747
; Publication No. US20060019336A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/10/950,747
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/782,587
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide tag
US-10-950-747-12

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 10
US-10-989-767A-698
; Sequence 698, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 511582005004
; CURRENT APPLICATION NUMBER: US/10/989,767A
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 698
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized 6-His tag
US-10-989-767A-698

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 11
US-10-903-612B-120
; Sequence 120, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Alex M.
; APPLICANT: Gilte, Sadanand
; APPLICANT: Berge, Vladislav B.
; APPLICANT: Rothschild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 120

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-903-612B-120
```

```
Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 12
US-10-857-435A-622
; Sequence 622, Application US/10857435A
; Publication No. US20060030007A1
; GENERAL INFORMATION:
; APPLICANT: Byrd, Devon R.N.
; APPLICANT: Esposito, Dominic
; APPLICANT: Potter, Robert Jason
; APPLICANT: Chappell, Thomas
; TITLE OF INVENTION: Peptides for Metal Ion Affinity Chromatography
; FILE REFERENCE: 0942.5790001
; CURRENT APPLICATION NUMBER: US/10/857,435A
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: 60/474,220
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 687
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 622
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-857-435A-622
```

```
Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 13
US-10-861-105-2
; Sequence 2, Application US/10861105
; Publication No. US20060035387A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Peter
; APPLICANT: Kernen, Peter
; APPLICANT: Lu, Hongbo
; APPLICANT: Tran, Huu
; APPLICANT: Zyomyx, Inc.
; TITLE OF INVENTION: Non-Specific Binding Resistant Protein Arrays and
; TITLE OF INVENTION: Methods for Making the Same
; FILE REFERENCE: 020144-001970US
; CURRENT APPLICATION NUMBER: US/10/861,105
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US/10/046,442
; PRIOR FILING DATE: 2001-10-27
; PRIOR APPLICATION NUMBER: US 09/115,455
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US09/353,555
; PRIOR FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: His-6 peptide
US-10-861-105-2
```

```
Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 14
US-10-968-629-13
; Sequence 13, Application US/10968629
; Publication No. US20060040382A1
; GENERAL INFORMATION:
; APPLICANT: Heflton et al.
; TITLE OF INVENTION: Tagged Epitope Protein Transposable Element
; FILE REFERENCE: 61589
; CURRENT APPLICATION NUMBER: US/10/968,629
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 09/979,338
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: PCT/US00/14687
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,210
; PRIOR FILING DATE: 1999-05-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of 6X
US-10-968-629-13
```

```
Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 15
US-10-498-665-72
; Sequence 72, Application US/10498665
; Publication No. US20060052292A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us620
; CURRENT APPLICATION NUMBER: US/10/498,665
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 6
```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide tag
US-10-498-665-72

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
DB 1 HHHHHH 6

RESULT 16
US-11-085-864-6
Sequence 6, Application US/11085864
Publication No. US20050246787A1
GENERAL INFORMATION:
APPLICANT: STRETFIELD, STEPHEN J.
APPLICANT: LOVE, ROBERT T.
APPLICANT: BRAY, JEFF
TITLE OF INVENTION: A GLOBULIN-1 REGULATORY REGION AND METHOD OF USING SAME
FILE REFERENCE: AB0002
CURRENT APPLICATION NUMBER: US/11/085,864
CURRENT FILING DATE: 2005-03-22
PRIOR APPLICATION NUMBER: 60/555,720
PRIOR FILING DATE: 2004-03-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-085-864-6

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
DB 1 HHHHHH 6

RESULT 17
US-11-158-848-35
Sequence 35, Application US/11158848
Publication No. US20050249703A1
GENERAL INFORMATION:
APPLICANT: Anne Dam Jensen
TITLE OF INVENTION: Interferon gamma polypeptide variants
FILE REFERENCE: 231us410 - INFG variants
CURRENT APPLICATION NUMBER: US/11/158,848
CURRENT FILING DATE: 2005-06-22
PRIOR APPLICATION NUMBER: US/10/116,273
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Tag
US-11-158-848-35

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
|||||
DB 1 HHHHHH 6

RESULT 18
US-11-040-159-21
Sequence 21, Application US/11040159
Publication No. US2005025552A1
GENERAL INFORMATION:
APPLICANT: Flynn, Peter
APPLICANT: Luehrsen, Kenneth
APPLICANT: Balint, Robert F.
APPLICANT: Her, Jeng-Horng
APPLICANT: Bebbington, Christopher R.
APPLICANT: Yarranton, Geoffrey T.
APPLICANT: Kalobios, Inc.
TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
FILE REFERENCE: 021167-001730US
CURRENT APPLICATION NUMBER: US/11/040,159
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 60/537,364
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/546,216
PRIOR FILING DATE: 2004-02-23
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6-His epitope tag
US-11-040-159-21

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
DB 1 HHHHHH 6

RESULT 19
US-11-040-114-9
Sequence 9, Application US/11040114
Publication No. US20050261170A1
GENERAL INFORMATION:
APPLICANT: HANSEN, HANS J.
APPLICANT: MCBRIDE, WILLIAM J.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: ROSSI, EDWARD A.
APPLICANT: CHANG, CHIEN-SHING KEN
TITLE OF INVENTION: FOLATE CONJUGATES AND COMPLEXES
FILE REFERENCE: 40923-0143US1
CURRENT APPLICATION NUMBER: US/11/040,114
CURRENT FILING DATE: 2005-01-24
PRIOR APPLICATION NUMBER: 60/538,396
PRIOR FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 9
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-040-114-9

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 20

US-11-073-605-16
; Sequence 16, Application US/11073605
; Publication No. US20050260161A1
; GENERAL INFORMATION:

; APPLICANT: ERIKSSON, ULF
; APPLICANT: ALITTAO, KARI
; APPLICANT: UTELA, MARCO
; TITLE OF INVENTION: METHOD FOR MODULATING REGULATING AND/OR STABILIZING
; FILE REFERENCE: 029065.53347US
; CURRENT APPLICATION NUMBER: US/11/073,605
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 60/550,327
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-073-605-16

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 21

US-11-102-428-8
; Sequence 8, Application US/11102428
; Publication No. US20050260164A1
; GENERAL INFORMATION:

; APPLICANT: OXFORD BIOMEDICA (UK) LIMITED
; TITLE OF INVENTION: GENE REGULATION WITH APTAMER AND MODULATOR COMPLEXES
; FILE REFERENCE: 674523-2031.WO
; CURRENT APPLICATION NUMBER: US/11/102,428
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/417,456
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 10/008,610
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/GB02/05901
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0130797.4
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: GB 0201140.1
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: GB 0211409.8
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 10/082,122
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 10/421,947

; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-102-428-8

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 22

US-11-127-004-4
; Sequence 4, Application US/11127004
; Publication No. US20050262596A1
; GENERAL INFORMATION:

; APPLICANT: STREARFIELD, STEPHEN J.
; APPLICANT: LOVE, ROBERT T.
; APPLICANT: BRAY, JEFF
; TITLE OF INVENTION: AN EMBRYO PREFERRED PROMOTER AND METHOD OF USING SAME
; FILE REFERENCE: AB0005
; CURRENT APPLICATION NUMBER: US/11/127,004
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: 60/570,665
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic six
US-11-127-004-4

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 23

US-11-000-365-46
; Sequence 46, Application US/11000365
; Publication No. US20050267022A1
; GENERAL INFORMATION:

; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: PAPA, SALVATORE
; APPLICANT: BUBICI, CONCETTA
; APPLICANT: DESABIELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
; FILE REFERENCE: 21459-97705
; CURRENT APPLICATION NUMBER: US/11/000,365
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/526,231
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 10/626,905

```

; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: 6xHis tag
US-11-000-365-46
```

```
Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
DB      1 HHHHHH 6
```

```

RESULT 24
US-11-032-794-46
; Sequence 46, Application US/11032794
; Publication No. US20050265970A1
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: PAPA, SALVATORE
; APPLICANT: BOBITI, CONCETTA
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
; TITLE OF INVENTION: CELL DEATH OR APOPTOSIS BY TARGETING JNK
; FILE REFERENCE: 21459-97816
; CURRENT APPLICATION NUMBER: US/11/032,794
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 11/000,365
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/526,231
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 10/626,905
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: 6xHis tag
US-11-032-794-46
```

```
Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
DB      1 HHHHHH 6
```

```

RESULT 25
US-11-097-749-40
; Sequence 40, Application US/11097749
; Publication No. US20050267028A1
; GENERAL INFORMATION:
; APPLICANT: VIRJI, MUMTAZ
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES
; FILE REFERENCE: 63221(50221)
; CURRENT APPLICATION NUMBER: US/11/097,749
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: GB0419594.7
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: GB0408390.3
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: GB2003/004273
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: GB0222764.3
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: 6xHis tag
US-11-097-749-40
```

```
Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
DB      1 HHHHHH 6
```

```

RESULT 26
US-11-006-031-20
; Sequence 20, Application US/11006031
; Publication No. US20050272114A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Keith V.
; APPLICANT: Klaubert, Dieter
; APPLICANT: Los, Georgy V.
; APPLICANT: Bulleit, Robert F.
; APPLICANT: McDougall, Mark
; APPLICANT: Zimprich, Chad
; APPLICANT: Promega Corporation
; TITLE OF INVENTION: Substrates for Covalent Tethering to Proteins
; FILE REFERENCE: 341.035U51
; CURRENT APPLICATION NUMBER: US/11/006,031
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 10/768,976
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,094
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/474,659
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/592,499
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-11-006-031-20
```

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 27

US-11-073-927-6
; Sequence 6, Application US/11073927
; Publication No. US20050271626A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN YUAN
; APPLICANT: SCOTT, MICHELE LYNN
; TITLE OF INVENTION: USE OF PROLACTIN RECEPTOR ANTAGONISTS IN COMBINATION
; TITLE OF INVENTION: WITH AN AGENT THAT INACTIVATES THE HER2/NEU SIGNALING
; FILE REFERENCE: 035679-0196
; CURRENT APPLICATION NUMBER: US/11/073,927
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 60/550,326
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-073-927-6

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 28

US-11-114-922-91
; Sequence 91, Application US/11114922
; Publication No. US20050282260A1
; GENERAL INFORMATION:
; APPLICANT: HICKS, PAULA M.
; APPLICANT: MCFAHLAN, SARA C.
; TITLE OF INVENTION: POLYPEPTIDES AND BIOSYNTHETIC PATHWAYS FOR THE
; TITLE OF INVENTION: PRODUCTION OF MONATIN AND ITS PRECURSORS
; FILE REFERENCE: 023829-0396
; CURRENT APPLICATION NUMBER: US/11/114,922
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/422,366
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/374,831
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 91
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-114-922-91

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 29

US-11-037-243-149
; Sequence 149, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: WHITE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 149
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: His tag
US-11-037-243-149

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 30

US-11-033-039-357
; Sequence 357, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 357
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-033-039-357

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 31

US-11-047-383-32
; Sequence 32, Application US/11047383
; Publication No. US20060003432A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; APPLICANT: BEATTIE, BRYAN
; APPLICANT: CLARKE, TERESA
; APPLICANT: KIMBER, MATTHEW
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM ENTEROCOCCUS FAECALIS
; FILE REFERENCE: IPT-318.01
; CURRENT APPLICATION NUMBER: US/11/047,383
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: PCT/CA03/01135
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/400,435
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 60/453,405
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 32
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-047-383-32

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 32

US-11-124-635-14
; Sequence 14, Application US/11124635
; Publication No. US20060003931A1
; GENERAL INFORMATION:
; APPLICANT: Eigenbrodt, Jr., Charles E.
; APPLICANT: Kirchhofer, Daniel K.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF THE HEPATOCYTE GROWTH FACTOR AND METHODS OF
; FILE REFERENCE: 11669.177USU1
; CURRENT APPLICATION NUMBER: US/11/124,635
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: US 60/569,301
; PRIOR FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Poly-His6 Tag

US-11-124-635-14

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 33

US-11-155-446-3
; Sequence 3, Application US/11155446
; Publication No. US20060003415A1
; GENERAL INFORMATION:
; APPLICANT: BATEMAN, ERIK
; TITLE OF INVENTION: STRABLE ACANTHAMOEBA PROTEIN EXPRESSION SYSTEMS
; FILE REFERENCE: 61243US(70360)
; CURRENT APPLICATION NUMBER: US/11/155,446
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/582,581
; PRIOR FILING DATE: 2004-06-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6x His
US-11-155-446-3

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 34

US-11-202-516-22
; Sequence 22, Application US/11202516
; Publication No. US20060008465A1
; GENERAL INFORMATION:
; APPLICANT: Steinaa, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gautam, Anand
; APPLICANT: Dalum, Iben
; APPLICANT: Haaning, Jesper
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; APPLICANT: Rasmussen, Peter
; TITLE OF INVENTION: Novel Methode for Therapeutic Vaccination
; FILE REFERENCE: 4614-0107PUS2
; CURRENT APPLICATION NUMBER: US/11/202,516
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US 09/806,703
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: PCT/DK99/00525
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: DK 1998 01261
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: US 60/105,011
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 6

```
/ TYPE: PRT
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION:
US-11-202-516-22
```

```
Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 35
US-11-008-570-129
/ Sequence 129, Application US/11008570
/ Publication No. US20060014162A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: CHAMOND, NATALIE
/ APPLICANT: MINOPRIO, PAOLA
/ APPLICANT: DEGRAVE, WIM M.
/ APPLICANT: BERREMAN, ARMAND
/ TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF RACEMASES,
/ TITLE OF INVENTION: DEFINITION OF PROTEIN SIGNATURES, AND A TEST FOR
/ TITLE OF INVENTION: DETECTING D-AMINO ACID AND FOR SCREENING MOLECULES
/ TITLE OF INVENTION: CAPABLE OF INHIBITING THE ACTIVITY OF RACEMASE,
/ TITLE OF INVENTION: ESPECIALLY PROLINE RACEMASE
/ FILE REFERENCE: 03495.0307-01
/ CURRENT APPLICATION NUMBER: US/11/008,570
/ CURRENT FILING DATE: 2004-12-10
/ PRIOR APPLICATION NUMBER: 10/775,339
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60-446,263
/ PRIOR FILING DATE: 2003-02-11
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 129
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-008-570-129
```

```
Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 36
US-11-056-182-19
/ Sequence 19, Application US/11056182
/ Publication No. US20060014245A1
/ GENERAL INFORMATION:
/ APPLICANT: GOLDENBERG, DAVID M.
/ APPLICANT: HANSEN, HANS J
/ APPLICANT: CHANG, CHIEH-HSING
/ APPLICANT: VANAMA, SAILAJA
/ APPLICANT: ROSSI, EDMUND A.
/ TITLE OF INVENTION: FUSION PROTEINS CONTAINING RECOMBINANT CYTOTOXIC RNASES
/ FILE REFERENCE: 40923-0002US1
/ CURRENT APPLICATION NUMBER: US/11/056,182
/ CURRENT FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: 60/544,227
/ PRIOR FILING DATE: 2004-02-13
/ NUMBER OF SEQ ID NOS: 22
```

```
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 19
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-056-182-19
```

```
Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 37
US-11-153-086-5
/ Sequence 5, Application US/11153086
/ Publication No. US20060014669A1
/ GENERAL INFORMATION:
/ APPLICANT: KOO, CALVIN
/ APPLICANT: MULLIGAN, RICHARD
/ TITLE OF INVENTION: A METHOD FOR TREATING CANCER AND INCREASING HEMATOOCRIT
/ TITLE OF INVENTION: LEVELS
/ FILE REFERENCE: 701039-51133-C
/ CURRENT APPLICATION NUMBER: US/11/153,086
/ CURRENT FILING DATE: 2005-06-15
/ PRIOR APPLICATION NUMBER: 10/467,509
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: PCT/US02/03531
/ PRIOR FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: 60/267,834
/ PRIOR FILING DATE: 2001-02-09
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 5
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6x
US-11-153-086-5
```

```
Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 38
US-11-121-612-400
/ Sequence 400, Application US/11121612
/ Publication No. US20060025339A1
/ GENERAL INFORMATION:
/ APPLICANT: The Procter & Gamble Company
/ APPLICANT: Isfort, Robert J
/ APPLICANT: Mazur, Wieslaw A
/ TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
/ FILE REFERENCE: 8847MD
/ CURRENT APPLICATION NUMBER: US/11/121,612
/ CURRENT FILING DATE: 2005-05-04
/ PRIOR APPLICATION NUMBER: US 60/349,117
/ PRIOR FILING DATE: 2002-01-16
/ PRIOR APPLICATION NUMBER: US 60/376,337
/ PRIOR FILING DATE: 2002-04-29
```

```

; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/317,252
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 531
; SOFTWARE: Patent version 3.3
; SEQ ID NO 400
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide sequence
US-11-121-612-400

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
   |||||
Db 1 HHHHH 6

RESULT 39
US-11-131-744-9
; Sequence 9, Application US/11131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHMOUD R.
; APPLICANT: POPE, ROBERT M.
; APPLICANT: SADEGHI, MEHRNOOSH
; APPLICANT: LIANG, XIQUAN
; APPLICANT: LEITE, JOHN F.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
; FILE REFERENCE: NVX-28 US
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/572,290
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/669,373
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/572,215
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/621,685
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: 60/621,686
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-9

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
   |||||
Db 1 HHHHH 6

RESULT 40
US-11-194-110-20
; Sequence 20, Application US/11194110
```

```

; Publication No. US20060024808A1
; GENERAL INFORMATION:
; APPLICANT: Darzins, AI
; APPLICANT: Encell, Lance
; APPLICANT: Klauber, Dieter
; APPLICANT: LoB, Georgy V.
; APPLICANT: McDougall, Mark
; APPLICANT: Wood, Keith V.
; APPLICANT: Wood, Monika G.
; APPLICANT: Zimprich, Chad
; APPLICANT: Promega Corporation
; TITLE OF INVENTION: Covalent Tethering of Functional Groups to Proteins and Substrat
; FILE REFERENCE: 341.032US1
; CURRENT FILING DATE: 2005-07-29
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-11-194-110-20

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
   |||||
Db 1 HHHHH 6

RESULT 41
US-11-051-178A-21
; Sequence 21, Application US/11051178A
; Publication No. US20060035296A1
; GENERAL INFORMATION:
; APPLICANT: TAYA, YOICHI
; APPLICANT: TAMAI, KATSUYUKI
; APPLICANT: MINAZAKI, TOSHIAKI
; TITLE OF INVENTION: METHOD FOR DETECTING ACETYLTRANSFERASE AND DEACETYLASE
; TITLE OF INVENTION: ACTIVITIES AND METHOD FOR SCREENING INHIBITORS OR
; FILE REFERENCE: 49979-DIV(71965)
; CURRENT FILING DATE: 2005-02-03
; PRIOR APPLICATION NUMBER: 09/618,424
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/JP99/00191
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: JP 10/9171
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-051-178A-21

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
   |||||
Db 1 HHHHH 6
```

RESULT 42
US-11-129-741-27
; Sequence 27, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KMOK YUNG
; APPLICANT: MOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KMOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-129-741-27

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||
Db 1 HHHHHH 6

RESULT 43
US-11-151-762-1
; Sequence 1, Application US/11151762
; Publication No. US20060035533A1
; GENERAL INFORMATION:
; APPLICANT: ZHAO, HUIMIN
; APPLICANT: WOODYER, RYAN
; APPLICANT: SIMURDIK, MICHAEL
; APPLICANT: VAN DER DONK, WILFRED A.
; TITLE OF INVENTION: A HIGHLY ACTIVE XYLOSE REDUCTASE FROM NEUROSPORA CRASSA
; FILE REFERENCE: 21419-99635
; CURRENT APPLICATION NUMBER: US/11/151,762
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,710
; PRIOR FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-151-762-1

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||

Db 1 HHHHHH 6

RESULT 44
US-11-108-088-71
; Sequence 71, Application US/11108088
; Publication No. US20060040353A1
; GENERAL INFORMATION:
; APPLICANT: DAVIDSON, ROBERT
; APPLICANT: GERNGROSS, TILLMAN
; APPLICANT: WILDT, STEFAN
; APPLICANT: CHOI, BYUNG-KWON
; APPLICANT: NETT, JUERGEN
; APPLICANT: BOBROWICZ, PIOTR
; APPLICANT: HAMILTON, STEPHEN
; TITLE OF INVENTION: PRODUCTION OF GALACTOSYLATED GLYCOPROTEINS IN LOWER
; TITLE OF INVENTION: EUKARYOTES
; FILE REFERENCE: GFI-12
; CURRENT APPLICATION NUMBER: US/11/108,088
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/214,358
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/215,638
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/279,997
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US02/41510
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 60/344,169
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/562,424
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 71
; LENGTH: 6
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6x
US-11-108-088-71

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||
Db 1 HHHHHH 6

RESULT 45
US-11-123-893-18
; Sequence 18, Application US/11123893
; Publication No. US20060041006A1
; GENERAL INFORMATION:
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: CHO, HANNA
; APPLICANT: ENGLAND, BRUCE
; APPLICANT: GILLETTE, SAM
; APPLICANT: ARTIS, DEAN RICHARD
; APPLICANT: ZUCKERMAN, REBECCA
; APPLICANT: ZHANG, CHAO
; TITLE OF INVENTION: PDE4B INHIBITORS AND USES THEREOF
; FILE REFERENCE: 039363-1109
; CURRENT APPLICATION NUMBER: US/11/123,893
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/569,435
; PRIOR FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18

```

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-123-893-18

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 46
US-11-179-363-29
; Sequence 29, Application US/11179363
; Publication No. US20060051841A1
; GENERAL INFORMATION:
; APPLICANT: GROSS, RICHARD W.
; TITLE OF INVENTION: IDENTIFICATION, CLONING, EXPRESSION, AND PURIFICATION
; TITLE OF INVENTION: OF THREE NOVEL HUMAN CALCIUM-INDEPENDENT PHOSPHOLIPASE
; TITLE OF INVENTION: A2 FAMILY MEMBERS POSSESSING TRIACYLGLYCEROL LIPASE AND
; FILE REFERENCE: 15060-76
; CURRENT APPLICATION NUMBER: US/11/179,363
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: 60/586,913
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 11/010,558
; PRIOR FILING DATE: 2004-12-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 29
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-179-363-29

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 47
US-11-108-001-13
; Sequence 13, Application US/11108001
; Publication No. US20050265962A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Steed, Paul Michael
; APPLICANT: Zalevsky, Jonathan
; APPLICANT: Szymkowski, David Edmund
; TITLE OF INVENTION: PROTEIN BASED TNF-ALPHA VARIANTS FOR THE TREATMENT OF TNF-ALPHA
; FILE REFERENCE: A-68990-7
; CURRENT APPLICATION NUMBER: US/11/108,001
; CURRENT FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 10/963,994
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 09/798,789
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/945,150
```

```

; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 09/981,289
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 10/262,630
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/553,908
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: US 60/510,430
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/509,960
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/528,275
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US 60/523,647
; PRIOR FILING DATE: 2003-11-20
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-11-108-001-13

Query Match          100.0%; Score 48; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 2 HHHHH 7

RESULT 48
US-11-222-451-21
; Sequence 21, Application US/11222451
; Publication No. US20060040356A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Gudarian, Jeffrey
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Methods of Using a Mycobacterium tuberculosis Coding
; TITLE OF INVENTION: Sequence to Facilitate Stable and High Yield Expression
; FILE REFERENCE: 014058-008010US
; CURRENT APPLICATION NUMBER: US/11/222,451
; CURRENT FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: US/09/684,215
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/158,585
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Met-His tag Gaa
US-11-222-451-21

Query Match          100.0%; Score 48; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 2 HHHHH 7

RESULT 49
```

Job time : 30 secs

US-10-950-747-13
; Sequence 13, Application US/10950747
; Publication No. US20060019336A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/10/950,747
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/782,587
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide tag
US-10-950-747-13

Query Match 100.0%; Score 48; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
DB 3 HHHHHH 8

RESULT 50
US-10-498-665-73
; Sequence 73, Application US/10498665
; Publication No. US20060052292A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilboud
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251ue620
; CURRENT APPLICATION NUMBER: US/10/498,665
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide tag
US-10-498-665-73

Query Match 100.0%; Score 48; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
DB 3 HHHHHH 8

Search completed: March 21, 2006, 11:12:57

THIS PAGE LEFT BLANK